

### Human Nucleic Acid Sequences from Hysteromyomic Tissue

The invention relates to human nucleic acid sequences from hysteromyomic tissue, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer in women is hysteromyoma, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations.

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They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this possibility of error can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52, which play a role as candidate genes in the hysteromyoma, have now been found.

Nucleic acid sequences Seq. ID Nos. 14-18, 30, 31 and 52 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 14-18, 30, 31 and 52.
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 14-18, 30, 31 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52, which are expressed elevated in the hysteromyoma.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 14-18, 30, 31 and 52.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 14-18, 30, 31 and 52 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs,  $\phi$ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Control or regulatory sequences are defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides, according to the sequence protocols ORF ID Nos. 32-51 and ORF ID Nos. 53-55.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of ORF ID Nos. 32-51 and ORF ID Nos. 53-55 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-31 and Seq. ID No. 52 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide

partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 32-51 and Seq. ID Nos. 53-55 according to the invention can also be used as tools for finding active ingredients against hysteromyoma, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52 for expression of polypeptides, which can be used as tools for finding active ingredients against hysteromyoma.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID No. 32 to Seq. ID No. 51 and Seq. ID Nos. 53-55 as pharmaceutical agents in the gene therapy for treatment of hysteromyoma or for the production of a pharmaceutical agent for treatment of hysteromyoma.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 32 to 51 and Seq. ID Nos. 53-55.

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The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID Nos. 1-31, and 52, and their use

together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-31 and 52, genomic BAC, PAC and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-31 and 52, for use as vehicles for gene transfer.

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### Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring amino acids

### Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

### Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

**Figure 3** shows the in-silico subtraction of gene expression in various tissues

**Figure 4a** shows the determination of tissue-specific expression via electronic Northern

**Figure 4b** shows the electronic Northern

**Figure 5** shows the isolation of genomic BAC and PAC clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

**Example 1**

**Search for Tumor-related Candidate Genes**

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the hystericomyomic tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

**Example 2****Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

**2.1. Electronic Northern Blot**

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) *J. Mol. Biol.* 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) *Nucleic Acids Research* 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) *Proc. Natl. Acad. Sci. USA* 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence  $S$ , e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence  $S$  which were determined in this way are called electronic Northern Blots.

## 2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 30 was found, which occurs more frequently in the hystero-myomic tissue than in normal tissue.

The result is as follows:

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09/673400

529 Rec'd PCT/PTC 17 OCT 2000

Electronic Northern for SEQ. ID NO.: 30

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0109	0.0021	5.1181	0.1954
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

**2.1.2.**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 31 was found, which occurs more frequently in the hysteromyomic tissue than in normal tissue.

The result is as follows:

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## Electronic Northern for SEQ. ID NO.: 31

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0104	0.2878	3.4745
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0111	0.0051	2.1599	0.4630
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0102	0.4064	2.4605
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0163	0.0068	2.3791	0.4203
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0224	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0061			
White blood cells	0.0213			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0082
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

In an analogous procedure, the following Northerns were also found:

Electronic Northern for SEQ. ID NO.: 1

	NORMAL % frequency	TUMOR % frequency	Ratios
			N/T      T/N
Bladder	0.0468	0.0562	0.8321 1.2018
Breast	0.0576	0.0752	0.7656 1.3062
Small intestine	0.0766	0.0662	1.1586 0.8631
Ovary	0.0509	0.0650	0.7829 1.2774
Endocrine tissue	0.0596	0.0702	0.8491 1.1778
Gastrointestinal	0.0690	0.1203	0.5735 1.7438
Brain	0.0850	0.0873	0.9741 1.0266
Hematopoietic	0.0722	0.0379	1.9056 0.5248
Skin	0.0918	0.0000	undef 0.0000
Hepatic	0.0143	0.1100	0.1298 7.7066
Heart	0.1123	0.0275	4.0862 0.2447
Testicles	0.0518	0.0819	0.6325 1.5809
Lung	0.1080	0.0879	1.2287 0.8138
Stomach-esophagus	0.0676	0.0307	2.2059 0.4533
Muscle-skeleton	0.0737	0.0780	0.9445 1.0587
Kidney	0.0407	0.0890	0.4575 2.1857
Pancreas	0.0463	0.0552	0.8376 1.1939
Penis	0.0449	0.0000	undef 0.0000
Prostate	0.0436	0.0554	0.7874 1.2700
Uterus-endometrium	0.0338	0.0000	undef 0.0000
Uterus-myometrium	0.0534	0.1426	0.3741 2.6732
Uterus-general	0.0255	0.0000	undef 0.0000
Breast hyperplasia	0.0863		
Prostate hyperplasia	0.0535		
Seminal vesicle	0.0890		
Sensory organs	0.0588		
White blood cells	0.0772		
Cervix	0.1171		

FETUS  
% frequency      STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0204
Gastrointestinal	0.0583	Ovary_n	0.1595
Brain	0.0500	Ovary_t	0.0051
Hematopoietic	0.0590	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0256
Hepatic	0.0000	Gastrointestinal	0.0488
Heart-blood vessels	0.0462	Hematopoietic	0.0000
Lung	0.0578	Skin-muscle	0.0227
Suprarenal gland	0.0254	Testicles	0.0154
Kidney	0.0679	Lung	0.0082
Placenta	0.0545	Nerves	0.0191
Prostate	0.2493	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

## Electronic Northern for SEQ. ID NO.: 2

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0102	0.3814	2.6222
Breast	0.0128	0.0038	3.4026	0.2939
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0075	0.2264	4.4166
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0022	0.0103	0.2160	4.6299
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0082	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0000	0.0408	0.0000	undef
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0384
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0259
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0328
Placenta	Nerves 0.0171
Prostate	Prostate 0.0137
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0083

## Electronic Northern for SEQ. ID NO.: 3

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.1103	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0140	0.0010	13.6792	0.0731
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0815	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix	0.0000	0.0000	undef	undef

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0090
Prostate	Prostate 0.0137
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

## Electronic Northern for SEQ. ID NO.: 4

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.1695	0.0000	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0095	0.0412	0.2313	4.3235
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0017	0.0077	0.0000	undef
Muscle-skeleton	0.0027	0.0120	0.1428	7.0040
Kidney	0.0033	0.0000	undef	0.0000
Pancreas	0.0030	0.0055	0.5983	1.6714
Penis	0.0000	0.0021	undef	0.0000
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0152	0.0883	0.1727	5.7919
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0068
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0093
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0130
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

## Electronic Northern for SEQ. ID NO.: 5

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder				
Breast	0.0390	0.0332	1.1734	0.8522
Small intestine	0.0345	0.0414	0.8352	1.1973
Ovary	0.0399	0.0662	0.6024	1.6599
Endocrine tissue	0.0359	0.0546	0.6579	1.5201
Gastrointestinal	0.0528	0.0351	1.5040	0.6649
Brain	0.0172	0.0185	0.9319	1.0731
Hematopoietic	0.0214	0.0359	0.5965	1.6763
Skin	0.0294	0.0379	0.7763	1.2881
Hepatic	0.0257	0.1695	0.1516	6.5954
Heart	0.0476	0.0323	1.4706	0.6800
Testicles	0.0276	0.0000	undef	0.0000
Lung	0.0633	0.0234	2.7059	0.3696
Stomach-esophagus	0.0312	0.0266	1.1724	0.8530
Muscle-skeleton	0.0387	0.0153	2.5211	0.3967
Kidney	0.0308	0.0360	0.8567	1.1673
Pancreas	0.0326	0.0548	0.5948	1.6813
Penis	0.0132	0.0221	0.5983	1.6714
Prostate	0.0479	0.0000	undef	0.0000
Uterus-endometrium	0.0153	0.0319	0.4777	2.0934
Uterus-myometrium	0.0473	0.0528	0.8962	1.1158
Uterus-general	0.0305	0.1019	0.2993	3.3415
Breast hyperplasia	0.0560	0.1908	0.2936	3.4065
Prostate hyperplasia	0.0448			
Seminal vesicle	0.1513			
Sensory organs	0.0235			
White blood cells	0.0061			
Cervix	0.0426			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0136
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0099
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0324
Suprarenal gland	Testicles	0.0231
Kidney	Lung	0.0328
Placenta	Nerves	0.0131
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0077
	Uterus_n	0.0208

## Electronic Northern for SEQ. ID NO.: 6

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0429	0.1278	0.3356	2.9798
Breast	0.1036	0.1203	0.8613	1.1610
Small intestine	0.0215	0.0992	0.2163	4.6240
Ovary	0.0599	0.0702	0.8528	1.1726
Endocrine tissue	0.0783	0.0426	1.8380	0.5441
Gastrointestinal	0.0249	0.0786	0.3167	3.1574
Brain	0.0429	0.1284	0.3341	2.9935
Hematopoietic	0.0227	0.1136	0.2000	5.0008
Skin	0.0844	0.1695	0.4982	2.0073
Hepatic	0.0523	0.0712	0.7353	1.3600
Heart	0.0922	0.1649	0.5590	1.7890
Testicles	0.0460	0.0585	0.7872	1.2704
Lung	0.0447	0.0797	0.5601	1.7853
Stomach-esophagus	0.0000	0.0537	0.0000	undef
Muscle-skeleton	0.1490	0.1380	1.0801	0.9258
Kidney	0.0489	0.0479	1.0196	0.9808
Pancreas	0.0149	0.1049	0.1417	7.0571
Penis	0.0509	0.1333	0.3819	2.6187
Prostate	0.0196	0.0319	0.6142	1.6282
Uterus-endometrium	0.0676	0.1583	0.4268	2.3432
Uterus-myometrium	0.0381	0.3260	0.1169	8.5541
Uterus-general	0.0560	0.0000	undef	0.0000
Breast hyperplasia	0.0863			
Prostate hyperplasia	0.0297			
Seminal vesicle	0.0089			
Sensory organs	0.0353			
White blood cells	0.0078			
Cervix	0.0213			

	FETUS % frequency
Development	
Gastrointestinal	0.1670
Brain	0.1444
Hematopoietic	0.0125
Skin	0.0629
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0889
Suprarenal gland	0.0759
Kidney	0.2535
Placenta	0.1112
Prostate	0.1091
Sensory organs	0.1247
	0.1004

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0476
Ovary_n	0.1595
Ovary_t	0.0203
Endocrine tissue	0.0000
Fetal	0.0379
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0486
Testicles	0.0077
Lung	0.0164
Nerves	0.0251
Prostate	0.0068
Sensory Organs	0.0155
Uterus_n	0.0167

## Electronic Northern for SEQ. ID NO.: 7

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0051	2.2882	0.4370
Breast	0.0128	0.0075	1.7013	0.5878
Small intestine	0.0153	0.0331	0.4634	2.1579
Ovary	0.0150	0.0104	1.4391	0.6949
Endocrine tissue	0.0085	0.0050	1.6981	0.5889
Gastrointestinal	0.0096	0.0278	0.3451	2.8974
Brain	0.0059	0.0113	0.5236	1.9098
Hematopoietic	0.0254	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0143	0.0194	0.7353	1.3600
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0058	0.0234	0.2460	4.0652
Lung	0.0104	0.0245	0.4234	2.3620
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0360	0.1428	7.0040
Kidney	0.0244	0.0068	3.5687	0.2802
Pancreas	0.0083	0.0000	undef	0.0000
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0218	0.0064	3.4121	0.2931
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0408	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0192	0.0030		
Prostate hyperplasia	0.0089	0.0089		
Seminal vesicle	0.0235	0.0235		
Sensory organs	0.0208	0.0208		
White blood cells	0.0213	0.0213		
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0093
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0342
Lung	Skin-muscle	0.0097
Suprarenal gland	Testicles	0.0154
Kidney	Lung	0.0082
Placenta	Nerves	0.0080
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0042

## Electronic Northern for SEQ. ID NO.: 8

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0460	0.6780	1.4750
Breast	0.0192	0.0282	0.6805	1.4694
Small intestine	0.0368	0.0000	undef	0.0000
Ovary	0.0210	0.0364	0.5756	1.7372
Endocrine tissue	0.0290	0.0326	0.8882	1.1258
Gastrointestinal	0.0460	0.0231	1.9880	0.5030
Brain	0.0532	0.0585	0.9094	1.0996
Hematopoietic	0.0361	0.0379	0.9528	1.0496
Skin	0.0367	0.0000	undef	0.0000
Hepatic	0.0048	0.0647	0.0735	13.5999
Heart	0.0699	0.0412	1.6961	0.5896
Testicles	0.0288	0.4210	0.0683	14.6349
Lung	0.0343	0.0368	0.9314	1.0737
Stomach-esophagus	0.0773	0.0230	3.3614	0.2975
Muscle-skeleton	0.0497	0.0660	0.7528	1.3283
Kidney	0.0353	0.1575	0.2241	4.4619
Pancreas	0.0165	0.0939	0.1760	5.6828
Penis	0.0299	0.0267	1.1232	0.8903
Prostate	0.0196	0.0298	0.6580	1.5197
Uterus-endometrium	0.0270	0.1583	0.1707	5.8579
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0505			
Seminal vesicle	0.0890			
Sensory organs	0.0353			
White blood cells	0.0399			
Cervix	0.0319			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0152
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0082
Hepatic	Gastrointestinal 0.0244
Heart-blood vessels	Hematopoietic 0.0057
Lung	Skin-muscle 0.0032
Suprarenal gland	Testicles 0.0077
Kidney	Lung 0.0082
Placenta	Nerves 0.0141
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0310
	Uterus_n 0.0125

## Electronic Northern for SEQ. ID NO.: 9

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0468	0.0204	2.2982	0.4370
Breast	0.0205	0.0451	0.4537	2.2042
Small intestine	0.0307	0.0331	0.9268	1.0789
Ovary	0.0539	0.0468	1.1513	0.8686
Endocrine tissue	0.0562	0.0527	1.0674	0.9369
Gastrointestinal	0.0249	0.0324	0.7692	1.3001
Brain	0.0333	0.0318	1.0451	0.9568
Hematopoietic	0.0388	0.0379	1.0234	0.9772
Skin	0.0257	0.1695	0.1516	6.5954
Hepatic	0.0095	0.0259	0.3676	2.7200
Heart	0.0540	0.0000	undef	0.0000
Testicles	0.0173	0.0702	0.2460	4.0652
Lung	0.0291	0.0491	0.5927	1.6872
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0206	0.1140	0.1803	5.5448
Kidney	0.0733	0.0274	2.6765	0.3736
Pancreas	0.0264	0.0331	0.7977	1.2536
Penis	0.0269	0.0533	0.5054	1.9786
Prostate	0.0501	0.0341	1.4715	0.6796
Uterus-endometrium	0.0541	0.2639	0.2049	4.8816
Uterus-myometrium	0.0152	0.0611	0.2494	4.0097
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0512			
Prostate hyperplasia	0.0386			
Seminal vesicle	0.0623			
Sensory organs	0.0470			
White blood cells	0.0286			
Cervix	0.0426			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0068
Gastrointestinal	Ovary_n	0.1595
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0256
Hepatic	Gastrointestinal	0.0732
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0551
Suprarenal gland	Testicles	0.0309
Kidney	Lung	0.0737
Placenta	Nerves	0.0231
Prostate	Prostate	0.0137
Sensory organs	Sensory Organs	0.0310
	Uterus_n	0.0333

## Electronic Northern for SEQ. ID NO.: 10

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1131	0.1431	0.7900	1.2659
Breast	0.1356	0.1692	0.8015	1.2476
Small intestine	0.1962	0.0165	11.8636	0.0843
Ovary	0.1827	0.2446	0.7471	1.3385
Endocrine tissue	0.1090	0.1329	0.8202	1.2192
Gastrointestinal	0.1878	0.2590	0.7248	1.3797
Brain	0.1035	0.1325	0.7814	1.2798
Hematopoietic	0.2700	0.1894	1.4257	0.7014
Skin	0.1358	0.0847	1.6028	0.6239
Hepatic	0.0428	0.1812	0.2363	4.2311
Heart	0.2586	0.0137	18.8118	0.0532
Testicles	0.0633	0.1403	0.4510	2.2174
Lung	0.3231	0.2229	1.4495	0.6899
Stomach-esophagus	0.1643	0.2147	0.7653	1.3066
Muscle-skeleton	0.1970	0.0960	2.0524	0.4872
Kidney	0.1222	0.2328	0.5248	1.9055
Pancreas	0.0876	0.1767	0.4955	2.0183
Penis	0.1407	0.1600	0.8798	1.1366
Prostate	0.1003	0.0766	1.3080	0.7645
Uterus-endometrium	0.1824	0.0528	3.4569	0.2893
Uterus-myometrium	0.1677	0.3804	0.4409	2.2681
Uterus-general	0.2292	0.0000	undef	0.0000
Breast hyperplasia	0.0735			
Prostate hyperplasia	0.0684			
Seminal vesicle	0.1335			
Sensory organs	0.0470			
White blood cells	0.2749			
Cervix	0.0958			

	FETUS % frequency
Development	
Gastrointestinal	0.0139
Brain	0.0639
Hematopoietic	0.1063
Skin	0.1258
Hepatic	0.2513
Heart-blood vessels	0.0260
Lung	0.0712
Suprarenal gland	0.1517
Kidney	0.0000
Placenta	0.0988
Prostate	0.0909
Sensory organs	0.1745
	0.0377

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0136
Ovary_n	0.3190
Ovary_t	0.0709
Endocrine tissue	0.0000
Fetal	0.0326
Gastrointestinal	0.1464
Hematopoietic	0.0000
Skin-muscle	0.1328
Testicles	0.0154
Lung	0.2211
Nerves	0.0311
Prostate	0.0410
Sensory Organs	0.0000
Uterus_n	0.0333

## Electronic Northern for SEQ. ID NO.: 11

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0051	3.0509	0.3278
Breast	0.0064	0.0113	0.5671	1.7633
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0240	0.0234	1.0233	0.9772
Endocrine tissue	0.0068	0.0100	0.6792	1.4722
Gastrointestinal	0.0096	0.0046	2.0708	0.4829
Brain	0.0022	0.0257	0.0864	11.5747
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0238	0.0065	3.6765	0.2720
Heart	0.0276	0.0275	1.0023	0.9977
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0083	0.0245	0.3387	2.9526
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0081	0.0616	0.1322	7.5658
Pancreas	0.0165	0.0000	undef	0.0000
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0065	0.0085	0.7677	1.3026
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0951	0.0802	12.4748
Uterus-general	0.0968	0.0000	undef	0.0000
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0706			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0233
Hepatic	Gastrointestinal	0.0244
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0648
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0164
Placenta	Nerves	0.0010
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0083

## Electronic Northern for SEQ. ID NO.: 12

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0351	0.3093	0.1135	8.8135
Breast	0.0269	0.0470	0.5716	1.7493
Small intestine	0.0092	0.0662	0.1390	7.1929
Ovary	0.0569	0.0182	3.1248	0.3200
Endocrine tissue	0.0528	0.0502	1.0528	0.9498
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0022	0.0873	0.0254	39.3541
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0220	0.5085	0.0433	23.0839
Hepatic	0.0285	0.0582	0.4902	2.0400
Heart	0.0191	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0114	0.0061	1.8628	0.5368
Stomach-esophagus	0.0193	0.0077	2.5211	0.3967
Muscle-skeleton	0.0771	0.0540	1.4278	0.7004
Kidney	0.0489	0.0137	3.5687	0.2802
Pancreas	0.0264	0.0442	0.5983	1.6714
Penis	0.0090	0.1066	0.0842	11.8713
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0743	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.1494	0.2551	3.9206
Uterus-general	0.0153	0.0954	0.1601	6.2452
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0612
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.1114
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.4665
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0030
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0291

## Electronic Northern for SEQ. ID NO.: 13

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
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Bladder				
Breast	0.0078	0.0204	0.3814	2.6222
Small intestine	0.0256	0.0432	0.5918	1.6899
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0060	0.0078	0.7675	1.3029
Gastrointestinal	0.0000	0.0050	0.0000	undef
Brain	0.0074	0.0216	0.3428	2.9168
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0115	0.0468	0.2460	4.0652
Lung	0.0031	0.0082	0.3810	2.6245
Stomach-esophagus	0.0580	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0300	0.0000	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0033	0.0276	0.1197	8.3571
Penis	0.0210	0.1066	0.1966	5.0877
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0883	0.3453	2.8959
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0356			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0639			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0408
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.1266
Hematopoietic	Endocrine tissue 0.0047
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0057
Heart-blood vessels	Hematopoietic 0.0032
Lung	Skin-Muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0030
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0208
	Uterus_n

## Electronic Northern for SEQ. ID NO.: 14

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder	0.0195	0.0051	3.8136	0.2622
Breast	0.0051	0.0132	0.3889	2.5715
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0150	0.0130	1.1513	0.8686
Endocrine tissue	0.0153	0.0150	1.0189	0.9815
Gastrointestinal	0.0115	0.0000	undef	0.0000
Brain	0.0133	0.0133	0.9969	1.0031
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0000	0.0194	0.0000	undef
Heart	0.0265	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0164	0.2540	3.9367
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0069	0.0540	0.1269	7.8795
Kidney	0.0217	0.0274	0.7930	1.2610
Pancreas	0.0165	0.0055	2.9915	0.3343
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0087	0.0170	0.5118	1.9538
Uterus-endometrium	0.0338	0.2111	0.1600	6.2484
Uterus-myometrium	0.0076	0.0475	0.1603	6.2374
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0238			
Prostate hyperplasia	0.0267			
Seminal vesicle	0.0000			
Sensory organs	0.0069			
White blood cells	0.0213			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0068
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0035
Hepatic	Gastrointestinal	0.0244
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0065
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0082
Placenta	Nerves	0.0050
Prostate	Prostate	0.0137
Sensory organs	Sensory Organs	0.0155
	Uterus_n	0.0042

## Electronic Northern for SEQ. ID NO.: 15

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0102	0.7627	1.3111
Breast	0.0026	0.0150	0.1701	5.8778
Small intestine	0.0184	0.0496	0.3707	2.6973
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0007	0.0072	0.1029	9.7228
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0086	0.0240	0.3569	2.8016
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0240	0.0000	undef	0.0000
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0096	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0139
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0039
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0249
Sensory organs	0.0000
Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0020
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0125
Uterus_n	

## Electronic Northern for SEQ. ID NO.: 16

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0153	0.2542	3.9333
Breast	0.0077	0.0038	2.0416	0.4898
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0119	0.0251	0.4755	2.1032
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0163	0.0246	0.6600	1.5152
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0180	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0135	0.0082	1.6511	0.6057
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0033	0.0276	0.1197	8.3571
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0196	0.0128	1.5354	0.6513
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0408	0.0000	undef
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0012
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0097
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0082
Placenta	Nerves	0.0050
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0083

## Electronic Northern for SEQ. ID NO.: 17

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0307	0.0338	0.9074	1.1021
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0509	0.0286	1.7792	0.5620
Endocrine tissue	0.0375	0.0301	1.2453	0.9030
Gastrointestinal	0.0153	0.0093	1.6567	0.6036
Brain	0.0222	0.0452	0.4909	2.0372
Hematopoietic	0.0160	0.0000	undef	0.0000
Skin	0.0661	0.0000	undef	0.0000
Hepatic	0.0143	0.0518	0.2757	3.6266
Heart	0.0636	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0177	0.0532	0.3322	3.0104
Stomach-esophagus	0.0483	0.0000	undef	0.0000
Muscle-skeleton	0.0137	0.0960	0.1428	7.0040
Kidney	0.0217	0.0685	0.3172	3.1524
Pancreas	0.0264	0.0055	4.7864	0.2089
Penis	0.0449	0.0000	undef	0.0000
Prostate	0.0283	0.0341	0.8317	1.2024
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0671			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0356			
Sensory organs	0.0353			
White blood cells	0.0121			
Cervix	0.0532			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0203
Hematopoietic	Endocrine tissue	0.0490
Skin	Fetal	0.0169
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0259
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0082
Placenta	Nerves	0.0050
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0167

## Electronic Northern for SEQ. ID NO.: 18

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0371	0.0357	1.0387	0.9627
Small intestine	0.0245	0.0331	0.7415	1.3487
Ovary	0.0479	0.0390	1.2280	0.8143
Endocrine tissue	0.0356	0.0326	1.0972	0.9114
Gastrointestinal	0.0153	0.0093	1.6567	0.6036
Brain	0.0229	0.0524	0.4376	2.2851
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0143	0.0518	0.2757	3.6266
Heart	0.0593	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0145	0.0491	0.2964	3.3743
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.1140	0.1052	9.5055
Kidney	0.0299	0.0616	0.4846	2.0634
Pancreas	0.0281	0.0055	5.0855	0.1966
Penis	0.0449	0.0000	undef	0.0000
Prostate	0.0349	0.0319	1.0919	0.9159
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0679	0.2245	4.4553
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0576			
Prostate hyperplasia	0.0446			
Seminal vesicle	0.0356			
Sensory organs	0.0235			
White blood cells	0.0130			
Cervix	0.0532			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0253
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0326
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0518
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0082
Placenta	Nerves	0.0090
Prostate	Prostate	0.0137
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0208

## Electronic Northern for SEQ. ID NO.: 19

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	Ratios T/N
Bladder				
Breast	0.0351	0.0332	1.0561	0.9469
Small intestine	0.0269	0.0376	0.7146	1.3995
Ovary	0.0337	0.0992	0.3398	2.9425
Endocrine tissue	0.0240	0.0312	0.7675	1.3029
Gastrointestinal	0.0409	0.0075	5.4340	0.1840
Brain	0.0268	0.0971	0.2761	3.6217
Hematopoietic	0.0059	0.0113	0.5236	1.9098
Skin	0.0013	0.2273	0.0059	170.0273
Hepatic	0.0330	0.0000	undef	0.0000
Heart	0.0095	0.0388	0.2451	4.0800
Testicles	0.0223	0.0000	undef	0.0000
Lung	0.0173	0.0351	0.4920	2.0326
Stomach-esophagus	0.0395	0.0900	0.4388	2.2792
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0857	0.1920	0.4462	2.2413
Pancreas	0.0136	0.0205	0.6609	1.5132
Penis	0.0198	0.0221	0.8974	1.1143
Prostate	0.0629	0.0800	0.7862	1.2719
Uterus-endometrium	0.0087	0.0106	0.8189	1.2211
Uterus-myometrium	0.0676	0.0000	undef	0.0000
Uterus-general	0.0686	0.1630	0.4208	2.3761
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0735			
Seminal vesicle	0.0416			
Sensory organs	0.0235			
White blood cells	0.0000			
Cervix	0.0426			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	
Gastrointestinal	0.1113
Brain	0.0056
Hematopoietic	0.0000
Skin	0.0039
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0289
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.1333
Prostate	0.0249
Sensory organs	0.0000
Breast	0.0204
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0111
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0000
Nerves	0.0068
Prostate	0.0077
Sensory Organs	0.0125
Uterus_n	

## Electronic Northern for SEQ. ID NO.: 20

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0858	0.1048	0.8185	1.2217
Breast	0.1036	0.1729	0.5992	1.6690
Small intestine	0.1226	0.1158	1.0593	0.9441
Ovary	0.0958	0.1197	0.8009	1.2486
Endocrine tissue	0.0954	0.1128	0.8453	1.1830
Gastrointestinal	0.0900	0.1573	0.5725	1.7466
Brain	0.0658	0.0924	0.7120	1.4046
Hematopoietic	0.1109	0.0758	1.4645	0.6828
Skin	0.0918	0.0000	undef	0.0000
Hepatic	0.0333	0.0906	0.3676	2.7200
Heart	0.2120	0.0412	5.1398	0.1946
Testicles	0.0690	0.3625	0.1904	5.2509
Lung	0.0696	0.1186	0.5869	1.7040
Stomach-esophagus	0.0483	0.0460	1.0504	0.9520
Muscle-skeleton	0.0702	0.2820	0.2491	4.0145
Kidney	0.0652	0.1027	0.6344	1.5762
Pancreas	0.1140	0.1270	0.8974	1.1143
Penis	0.1018	0.0000	undef	0.0000
Prostate	0.1149	0.0000	undef	0.0000
Uterus-endometrium	0.0686	0.2106	0.3258	3.0692
Uterus-myometrium	0.0458	0.1908	0.2402	4.1635
Uterus-general	0.1279			
Breast hyperplasia	0.1159			
Prostate hyperplasia	0.1157			
Seminal vesicle	0.1059			
Sensory organs	0.0832			
White blood cells	0.1278			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0136
Gastrointestinal	0.0557	Ovary_n	0.1595
Brain	0.2471	Ovary_t	0.0658
Hematopoietic	0.2189	Endocrine tissue	0.0000
Skin	0.1612	Fetal	0.0216
Hepatic	0.0000	Gastrointestinal	0.0732
Heart-blood vessels	0.1560	Hematopoietic	0.0057
Lung	0.2633	Skin-muscle	0.0259
Suprarenal gland	0.1012	Testicles	0.0000
Kidney	0.1014	Lung	0.1638
Placenta	0.1112	Nerves	0.0211
Prostate	0.0848	Prostate	0.0205
Sensory organs	0.3740	Sensory Organs	0.0000
	0.0126	Uterus_n	0.0333

## Electronic Northern for SEQ. ID NO.: 21

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0273	0.0102	2.6695	0.3746
Breast	0.0051	0.0019	2.7221	0.3674
Small intestine	0.0276	0.0000	undef	0.0000
Ovary	0.0180	0.0000	undef	0.0000
Endocrine tissue	0.0136	0.0000	undef	0.0000
Gastrointestinal	0.0134	0.0046	2.8992	0.3449
Brain	0.0015	0.0164	0.0900	11.1117
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0106	0.0412	0.2570	3.8912
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0052	0.0102	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0223	0.0060	3.7122	0.2694
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0033	0.0276	0.1197	8.3571
Penis	0.0030	0.0267	0.1123	8.9035
Prostate	0.0022	0.0043	0.9118	1.9538
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.1019	0.3741	2.6732
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0130			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development		
Gastrointestinal	0.0000	Breast 0.0204
Brain	0.0111	Ovary_n 0.0000
Hematopoietic	0.0000	Ovary_t 0.0101
Skin	0.0157	Endocrine tissue 0.0490
Hepatic	0.0000	Fetal 0.0093
Heart-blood vessels	0.0000	Gastrointestinal 0.0122
Lung	0.0107	Hematopoietic 0.0057
Suprarenal gland	0.0000	Skin-muscle 0.0421
Kidney	0.0000	Testicles 0.0154
Placenta	0.0247	Lung 0.0000
Prostate	0.0000	Nerves 0.0010
Sensory organs	0.0000	Prostate 0.0274
	0.0000	Sensory Organs 0.0000
		Uterus_n 0.0000

## Electronic Northern for SEQ. ID NO.: 22

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
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Bladder				
Breast	0.0000	0.0102	0.0000	undef
Small intestine	0.0064	0.0207	0.3093	3.2328
Ovary	0.0153	0.0662	0.2317	4.3157
Endocrine tissue	0.0180	0.0156	1.1513	0.8686
Gastrointestinal	0.0204	0.0351	0.5822	1.7176
Brain	0.0153	0.0231	0.6627	1.5090
Hematopoietic	0.0510	0.0257	1.9871	0.5032
Skin	0.0134	0.0000	undef	0.0000
Hepatic	0.0367	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0466	0.0000	undef	0.0000
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0249	0.0348	0.7172	1.3943
Muscle-skeleton	0.0193	0.0077	2.5211	0.3967
Kidney	0.0377	0.0300	1.2564	0.7959
Pancreas	0.0244	0.0274	0.8922	1.1209
Penis	0.0083	0.0166	0.4986	2.0057
Prostate	0.0329	0.0267	1.2355	0.8094
Uterus-endometrium	0.0131	0.0149	0.8774	1.1397
Uterus-myometrium	0.0338	0.0000	undef	0.0000
Uterus-general	0.0000	0.0340	0.0000	undef
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0256			
Seminal vesicle	0.0238			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0069			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.3190
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0373
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0114
Lung	Skin-muscle	0.0680
Suprarenal gland	Testicles	0.0231
Kidney	Lung	0.0000
Placenta	Nerves	0.0211
Prostate	Prostate	0.0205
Sensory organs	Sensory Organs	0.0077
	Uterus_n	0.0458

## Electronic Northern for SEQ. ID NO.: 23

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0741	0.0639	1.1593	0.8626
Breast	0.0691	0.0827	0.8352	1.1973
Small intestine	0.0245	0.0496	0.4943	2.0230
Ovary	0.0689	0.0494	1.3936	0.7176
Endocrine tissue	0.2487	0.5191	0.4791	2.0873
Gastrointestinal	0.0421	0.0879	0.4796	2.0852
Brain	0.1700	0.1037	1.6395	0.6099
Hematopoietic	0.0695	0.0758	0.9175	1.0899
Skin	0.0367	0.4237	0.0866	11.5419
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0668	0.1375	0.4857	2.0588
Testicles	0.0460	0.0468	0.9839	1.0163
Lung	0.0592	0.0470	1.2590	0.7943
Stomach-esophagus	0.1160	0.0690	1.6807	0.5950
Muscle-skeleton	0.0754	0.0960	0.7853	1.2735
Kidney	0.0706	0.0479	1.4728	0.6790
Pancreas	0.0677	0.0552	1.2265	0.8153
Penis	0.0988	0.0267	3.7064	0.2698
Prostate	0.0697	0.0660	1.0566	0.9464
Uterus-endometrium	0.0608	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0611	0.2494	4.0097
Uterus-general	0.1120	0.0000	undef	0.0000
Breast hyperplasia	0.0480	0.0565		
Prostate hyperplasia		0.0445		
Seminal vesicle		0.0823		
Sensory organs		0.0824		
White blood cells		0.0852		
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0544
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0203
Hematopoietic	Endocrine tissue 0.0245
Skin	Fetal 0.0309
Hepatic	Gastrointestinal 0.0610
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0356
Suprarenal gland	Testicles 0.0077
Kidney	Lung 0.0655
Placenta	Nerves 0.0783
Prostate	Prostate 0.0547
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0083

## Electronic Northern for SEQ. ID NO.: 24

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0546	0.0332	1.6428	0.6087
Breast	0.0269	0.0320	0.8407	1.1896
Small intestine	0.0276	0.0000	undef	0.0000
Ovary	0.0479	0.0546	0.8771	1.1401
Endocrine tissue	0.0324	0.0176	1.8437	0.5424
Gastrointestinal	0.0211	0.0463	0.4556	2.1950
Brain	0.0229	0.0277	0.8266	1.2097
Hematopoietic	0.0348	0.0379	0.9175	1.0899
Skin	0.0194	0.0000	undef	0.0000
Hepatic	0.0190	0.0000	undef	0.0000
Heart	0.0477	0.0000	undef	0.0000
Testicles	0.0230	0.1169	0.1968	5.0816
Lung	0.0156	0.0307	0.5080	1.9684
Stomach-esophagus	0.0000	0.0460	0.0000	undef
Muscle-skeleton	0.0120	0.0480	0.2499	4.0023
Kidney	0.0163	0.0068	2.3791	0.4203
Pancreas	0.0182	0.0331	0.5484	1.8234
Penis	0.0180	0.0800	0.2246	4.4517
Prostate	0.0174	0.0170	1.0236	0.9769
Uterus-endometrium	0.0541	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0576			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0277			
Cervix	0.0213			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0006
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0000
Placenta	Nerves	0.0040
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 25

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0429	0.0486	0.8832	1.1323
Breast	0.0435	0.0771	0.5643	1.7720
Small intestine	0.0307	0.0000	undef	0.0000
Ovary	0.0389	0.0833	0.4677	2.1381
Endocrine tissue	0.0460	0.0301	1.5283	0.6543
Gastrointestinal	0.0287	0.0971	0.2958	3.3803
Brain	0.0347	0.0534	0.6507	1.5367
Hematopoietic	0.0869	0.0000	undef	0.0000
Skin	0.0551	0.0847	0.6498	1.5389
Hepatic	0.0143	0.0194	0.7353	1.3600
Heart	0.0466	0.0137	3.3923	0.2948
Testicles	0.0173	0.0935	0.1845	5.4203
Lung	0.0457	0.0613	0.7451	1.3421
Stomach-esophagus	0.0290	0.0153	1.8908	0.5289
Muscle-skeleton	0.0223	0.1140	0.1954	5.1183
Kidney	0.0407	0.0137	2.9739	0.3363
Pancreas	0.0314	0.0442	0.7105	1.4075
Penis	0.0779	0.0533	1.4601	0.6849
Prostate	0.0458	0.0617	0.7412	1.3491
Uterus-endometrium	0.0473	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.1087	0.2806	3.5642
Uterus-general	0.0357	0.0954	0.3736	2.6765
Breast hyperplasia	0.0256			
Prostate hyperplasia	0.0803			
Seminal vesicle	0.0801			
Sensory organs	0.0118			
White blood cells	0.0494			
Cervix	0.0426			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0204
Gastrointestinal	Ovary_n	0.1595
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0332
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0194
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0328
Placenta	Nerves	0.0161
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0291

## Electronic Northern for SEQ. ID NO.: 26

	NORMAL % frequency	TUMOR % frequency	Ratios	
			N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	3.0675	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0070
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0155
Sensory organs	Sensory Organs 0.0250
	Uterus_n

Electronic Northern for SEQ. ID NO.: 27

NORMAL		TUMOR		Ratios	
% frequency	% frequency			N/T	T/N

Bladder	0.0039	0.0230	0.1695	5.8999
Breast	0.0179	0.0395	0.4537	2.2042
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0300	0.0130	2.3025	0.4343
Endocrine tissue	0.0068	0.0251	0.2717	3.6805
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0015	0.0092	0.1600	6.2504
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0194	0.0000	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0368	0.2258	4.4288
Stomach-esophagus	0.0290	0.0230	1.2605	0.7933
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0136	0.0068	1.9826	0.5044
Pancreas	0.0000	0.0276	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0128	0.5118	1.9538
Uterus-endometrium	0.0473	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0000		
Prostate hyperplasia	0.0030	0.0089		
Seminal vesicle	0.0000	0.0000		
Sensory organs	0.0000	0.0213		
White blood cells	0.0000	0.0000		
Cervix	0.0000	0.0000		

FETUS	STANDARDIZED/SUBTRACTED LIBRARIES
% frequency	% frequency

Development		Breast	
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0278	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0304
Skin	0.0079	Fetal	0.0245
Hepatic	0.0000	Gastrointestinal	0.0029
<u>Heart-blood vessels</u>	0.0000	Hematopoietic	0.0122
Lung	0.0320	Skin-muscle	0.0114
Suprarenal gland	0.0289	Testicles	0.0097
Kidney	0.0000	Lung	0.0000
Placenta	0.0185	Nerves	0.0164
Prostate	0.0000	Prostate	0.0020
Sensory organs	0.0997	Sensory Organs	0.0068
	0.0000	Uterus_n	0.0000

## Electronic Northern for SEQ. ID NO.: 28

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0383	0.5085	1.9666
Breast	0.0256	0.0714	0.3582	2.7919
Small intestine	0.0552	0.0331	1.6683	0.5994
Ovary	0.0270	0.0468	0.5756	1.7372
Endocrine tissue	0.0477	0.0451	1.0566	0.9464
Gastrointestinal	0.0326	0.0324	1.0058	0.9942
Brain	0.0503	0.0277	1.8132	0.5515
Hematopoietic	0.0201	0.1894	0.1059	9.4460
Skin	0.0367	0.2542	0.1444	6.9252
Hepatic	0.0476	0.0388	1.2255	0.8160
Heart	0.0699	0.0550	1.2721	0.7861
Testicles	0.0173	0.1403	0.1230	8.1305
Lung	0.0395	0.0818	0.4826	2.0720
Stomach-esophagus	0.0676	0.0613	1.1030	0.9066
Muscle-skeleton	0.0394	0.0300	1.3135	0.7613
Kidney	0.0462	0.0616	0.7490	1.3351
Pancreas	0.0347	0.0607	0.5711	1.7510
Penis	0.0509	0.1600	0.3182	3.1424
Prostate	0.0327	0.0149	2.1935	0.4559
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0543	0.1403	7.1284
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0565			
Seminal vesicle	0.0445			
Sensory organs	0.0941			
White blood cells	0.0390			
Cervix	0.0319			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development		
Gastrointestinal	0.0557	Breast 0.0340
Brain	0.0194	Ovary_n 0.0000
Hematopoietic	0.0188	Ovary_t 0.0101
Skin	0.0197	Endocrine tissue 0.0000
Hepatic	0.0000	Fetal 0.0396
Heart-blood vessels	0.0000	Gastrointestinal 0.0244
Lung	0.0320	Hematopoietic 0.0000
Suprarenal gland	0.0325	Skin-muscle 0.0778
Kidney	0.0000	Testicles 0.0000
Placenta	0.0371	Lung 0.0000
Prostate	0.0242	Nerves 0.0231
Sensory organs	0.0997	Prostate 0.0479
	0.0000	Sensory Organs 0.0697
		Uterus_n 0.0291

## Electronic Northern for SEQ. ID NO.: 29

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0663	0.0358	1.8523	0.5399
Breast	0.0512	0.0489	1.0470	0.9551
Small intestine	0.0368	0.0496	0.7415	1.3487
Ovary	0.0779	0.0728	1.0690	0.9354
Endocrine tissue	0.0562	0.0326	1.7242	0.5800
Gastrointestinal	0.0345	0.0370	0.9319	1.0731
Brain	0.0392	0.0524	0.7482	1.3366
Hematopoietic	0.0602	0.0379	1.5880	0.6297
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0095	0.0647	0.1471	6.7999
Heart	0.0583	0.0550	1.0601	0.9433
Testicles	0.0173	0.1520	0.1135	8.8080
Lung	0.0208	0.0491	0.4234	2.3620
Stomach-esophagus	0.0387	0.0460	0.8404	1.1900
Muscle-skeleton	0.0160	0.0420	0.8567	1.1673
Kidney	0.0380	0.0616	0.6168	1.6213
Pancreas	0.0314	0.0884	0.3552	2.8150
Penis	0.0689	0.0267	2.5833	0.3871
Prostate	0.0436	0.0490	0.8901	1.1235
Uterus-endometrium	0.0541	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.1155	0.3301	3.0296
Uterus-general	0.0815	0.0000	undef	0.0000
Breast hyperplasia	0.0831			
Prostate hyperplasia	0.0446			
Seminal vesicle	0.0801			
Sensory organs	0.0353			
White blood cells	0.0520			
Cervix	0.0532			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.1595
Brain	Ovary_t	0.0203
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0093
Hepatic	Gastrointestinal	0.0366
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0130
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0164
Placenta	Nerves	0.0120
Prostate	Prostate	0.0205
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0208

## Electronic Northern for SEQ. ID NO.: 30

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0109	0.0021	5.1181	0.1954
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0068
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n

## Electronic Northern for SEQ. ID NO.: 31

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0104	0.2878	3.4745
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0111	0.0051	2.1599	0.4630
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0102	0.4064	2.4605
Stomach-esophagus	0.0034	0.0060	undef	undef
Muscle-skeleton	0.0163	0.0068	0.5711	1.7510
Kidney	0.0017	0.0000	2.3791	0.4203
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0022	0.0021	undef	0.0000
Prostate	0.0135	0.0000	1.0236	0.9769
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0224			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0061			
White blood cells	0.0213			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0082
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

## Electronic Northern for Seq. ID: 52

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0599	0.0543	1.1037 0.9060
Breast	0.0507	0.0282	1.7979 0.5562
Large intestine	0.0326	0.0450	0.7240 1.3811
Small intestine	0.0268	0.0313	0.8563 1.1679
Ovary	0.0439	0.0426	1.0306 0.9703
Endocrine tissue	0.0564	0.0453	1.2443 0.8037
Brain	0.0642	0.0530	1.2113 0.8255
Skin	0.0380	0.0379	1.0022 0.9978
Hepatic	0.0330	0.0789	0.4190 2.3868
Heart	0.0093	0.0508	0.1831 5.4614
Testicles	0.0589	0.0000	undef 0.0000
Lung	0.0482	0.0533	0.9047 1.1054
Stomach-esophagus	0.0389	0.0499	0.7796 1.2828
Muscle-skeleton	0.0072	0.0256	0.2833 3.5296
Kidney	0.0240	0.0702	0.3418 2.9256
Pancreas	0.0694	0.0289	2.3984 0.4169
Prostate	0.0297	0.0331	0.8974 1.1143
T lymphoma	0.0443	0.0287	1.5457 0.6470
Uterus	0.0505	0.1643	0.3074 3.2533
White blood cells	0.0325	0.0690	0.4715 2.1210
Hematopoietic	0.0363	0.0304	1.1948 0.8370
Penis	0.0495		
Seminal vesicle	0.0322		
Sensory organs	0.0493		
	0.0470		

FETUS  
% freq.

Development	0.0696
Gastrointestinal	0.0750
Brain	0.0876
Hematopoietic	0.0904
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0854
Lung	0.0867
Adrenal gland	0.0761
Kidney	0.0556
Placenta	0.0606
Prostate	0.0499
Sensory organs	0.0628

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	
Breast_t	0.0068
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.1595
Endocrine tissue	0.0101
Fetal	0.0245
Gastrointestinal	0.0284
Hematopoietic	0.0732
Skin-muscle	0.0000
Testicles_n	0.0616
Testicles_t	0.0293
Lungs_n	0.0000
Lungs_t	0.0195
Nerves	0.0000
Kidney_t	0.0261
Ovary_Uterus	0.0000
Prostate_n	0.0293
Sensory_organs	0.0121
White blood cells	0.0310
	0.0000

## 2.2. Fisher Test

In order to decide whether a partial sequence  $S$  of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) *Statistics*, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to  $S$ . If the null hypothesis can be rejected with high enough certainty, the gene belonging to  $S$  is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

### Example 3

#### Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence  $S$  is completed in three steps:

1. Determination of all sequences homologous to  $S$  from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence  $C$  from the assembled sequences.

Consensus sequence  $C$  will generally be longer than initial sequence  $S$ . Its electronic Northern Blot will accordingly

deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences  $C_i$  (i: iteration index) obtained in each case until the alternative hypothesis is rejected (if  $H_0$  Exit; truncation criterion I) or until automatic lengthening is no longer possible (while  $C_i > C_{i-1}$ ; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from hysteromyomic tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

**Example 4****Mapping of Nucleic Acid Sequences on the Human Genome**

*Sub  
D1*

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server ([http://www.stanford.edu/RH/rhserver\\_form2.html](http://www.stanford.edu/RH/rhserver_form2.html)). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

**DOVER LIBRARIES**

the results were evaluated with the above-mentioned software and  
the software of the Whitehead Institute  
(<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

By  
Cont

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**TABLE I**

Col. 1 - Sequence ID No.:

Col. 2 - Expression in hysteromyomic/tissue:

Col. 3 - Function

Col. 4 - Modules

Col. 5 - Length of the applied sequence in bases

Col. 6 - Cytogenetic localization

Col. 7 - Next marker

[Key to Table I:]

[Col. 2:] erhöht = elevated

[Col. 3:]

[Seq. ID No.: 14, 15, 17, 30, 31] unbekannt = unknown

[Seq. ID No.: 16] Homolog zu Homo sapiens... = homologous to homo sapiens...

[Seq. ID No.: 18] Humanes Homolog zu ... = human homolog to

[Seq. ID No.: 52] Verlängerung von Seq. ID. 14 = Lengthening of Seq. ID. 14

TABELLE I

TABLE I

Sequenz ID No.:	Expression im Uterus-Myomgewebe:	Funktion	Module	Länge der angenommenen Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
1	erhöht	Human mRNA for ornithine decarboxylase antizyme	"aathydro-lase"	779		
2	erhöht	Human MEST mRNA		2310		D5S1730
3	erhöht	Human cocaine and amphetamine regulated transcript CART (hCART)		854	5q11.2-q13.1	
4	erhöht	Human microfibril-associated glycoprotein (MFAP2)		1112	1p36.11-p36.13	D2S387
5	erhöht	Human mRNA for KIAA0108 gene		1051	2p23.3	
6	erhöht	Human SPARC/osteonectin	"kazal"	1516	5q32-q33.1	
7	erhöht	Homo sapiens splicing factor, arginine/serine-rich 7 (SFRS7)	"rrm"	2367	2p22.3-p22.1	WI-9798
8	erhöht	Human triosephosphate isomerase	3x "TIM"	568		
9	erhöht	Human nuclear ribonucleoprotein particle (hnRNP) C		1775		
10	erhöht	Human thymosin beta-4	"Thymosin"	509		
11	erhöht	Human growth hormone-dependent insulin-like growth factor-binding protein mRNA	"IGFBP", "thyro-globulin_1"	2191	7p12.2-p13	
12	erhöht	Human H19	"lipocalin"	1026		
13	erhöht	Human cellular retinolic acid-binding protein II (CRABP)	"rrm"	676	14p11.2-14p11.1	WI-4204
14	erhöht	unbekannt		1254		
15	erhöht	unbekannt		537		
16	erhöht	Homolog zu Homo sapiens mRNA for putatively prenylated protein		823		
17	erhöht	unbekannt		1882		
18	erhöht	Humanes Homolog zu <i>P. vivax</i> pva1 gene	5x "LRR"	1548	12q21.31-12q21.33	D12S351
19	erhöht	Human lumican mRNA	"S2"	844		
20	erhöht	Human 37 kD laminin receptor precursor/p40 ribosome associated protein				
21	erhöht	Human YMP	"PMP22"	862		
22	erhöht	Human NADH-ubiquinone oxidoreductase MLRQ subunit	"G-alpha", "arf"	546		
23	erhöht	Human mRNA for coupling protein G(s) alpha-subunit	"rrm"	1591	20q13.32-q13.33	
24	erhöht	Human hnRNP core protein A1	"rrm"	441		
25	erhöht	Human HMG-17 gene for non-histone chromosomal protein	"HMG14_17"	1131		
26	erhöht	H. sapiens mRNA for protaclin (clone PR1205)	"hormone"	1071		
27	erhöht	Human mRNA for neutrophil outgrowth-promoting protein.	"PTN_MK"	3x	896	
28	erhöht	H. sapiens mRNA for proliferation-associated gene (pag)	"AlpC-TSA"	1050	1p32.3-p34.3	
29	erhöht	H. sapiens alpha NAC		581		
30	erhöht	unbekannt		264		
31	erhöht	unbekannt		111		
52	erhöht	Verlängerung von Seq. ID. 14	"rrm"	3665	14p11.2-14p11.1	WI-4204

References to the modules:

Pfam: Protein families database of alignments and HMMs  
(pfam@sanger.ac.uk)

PROSITE: The PROSITE database, its status in 1999. Nucleic  
Acids Res. 27: 215-219 (<http://www.expasy.ch/sprot/prosite.html>)

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TABLE II

DNA Sequences	Peptide Sequences (ORF's)
Seq. ID. No.	Seq. ID. No.
14	32
	33
	34
15	35
	36
	37
16	38
	39
17	40
	41
	42
18	43
	44
	45
30	46
	47
31	48
	49
	50
	51
52	53
	54
	55

09673400-42200

The inventive nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 of the determined candidate genes and the determined amino acid sequences Seq. ID No. 32 to Seq. ID No. 51 are described in the following sequence protocol.

### **Sequence Protocol**

#### **(1) GENERAL INFORMATION:**

##### **(i) APPLICANT:**

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Hysteromyomic Tissue

(iii) Number of sequences: 55

##### **(iv) COMPUTER READABLE FORM:**

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

(2) INFORMATION ON SEQ ID NO. 1:

(i) SEQUENCE CHARACTERISTIC

- (A) LENGTH: 779 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

agcgagcagc ggcggcggcg cggagagacg cagcggaggt tttctgggt tcggaccca 60  
gcggccggat ggtgaaatcc tccctgcgcg ggatcctcaa tagccactgc ttcgcccagag 120  
agaaggaagg ggataaaccg agcgccacca tccacgcccag cccgaccatg ccgctccctaa 180  
gcctgcacacg cccgccccggc agcagcagtg agagttccag ggtctccctc cactgctgt 240  
gtaacccggg tccggggcct cgggtgggtct cctgatgccc ctcacccacc cctgaagatc 300  
ccaggtgggc gagggaatag tcaaaggac cacaatctt cagctaactt attctactcc 360  
gatgatcgcc tgaatgtAAC agaggaacta acgtccaaacg acaagacgag gattctcaac 420  
gtccagtcctt ggctcacaga cgccaaacgc attaactggc gaacagtgt gaggggcggc 480  
actgctctac atcgagatcc cgggcggcgc gctgcccggq gggagcaagg acagcttgc 540  
agttctctcg ggagttcgct gaggagcgc tgcgaggccc accatgtctt aatttgcctc 600  
cacaagaacc cccgaggacag agccgccttgc ctccqaaacct tcagctttt cgggcttgag 660  
attttgagac cggggcatcc cttttgttcc ccaagagacc cgacqcttgc ttcatggggc 720  
tacaagtttcc gagagagagt ctttggggagq aggaagaagg attaagggccc qcqtcggqgt 779

(2) INFORMATION ON SEQ ID NO. 2:

**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 2310 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

gttctccgaa	acatggagtc	ctgttaaggcaa	ggtctttaccc	gaatcaggat	gaggggagtg	60
tgggtccagg	tggggctgct	ggccgtgccc	ctgttttgctg	cgtacctgca	catcccccc	120
cctcagcgct	ccccctgcccc	tcactctatgg	aagtcttcag	gcaagttttt	cacttacaag	180
ggactcgcta	tcttcttacca	agactctgtg	ggtgtggtg	gaagttccaga	gatagttgtg	240
cttttacacg	gttttccaaac	atccagctac	gactggata	agatttggga	aggctgtgacc	300
ttgagggtttc	atcggtgtat	tgcctttaggt	ttctttaggt	ttggcttcag	tgacaaaccg	360
agaccacatc	actattccat	atttgagcag	gccagcatcg	tggaaagcgct	tttgccggcat	420
ctggggctcc	agaaccgcag	gatcaaccc	ctttctcatg	actatggaga	tattgttgt	480
caggagcttc	tctacaggtt	caagcagaat	cgatctggc	ggcttaccat	aaagagtttc	540
tgtctgtcaa	atggaggtat	cttgcctgag	actcaccgtc	cactccctct	ccaaaagcta	600
ctcaaagatg	gaggtgtgt	gtcaccatc	ctcacacgac	tgtatgactt	ctttgtattc	660
tctcgaggtc	tcaccccaat	cttggggccg	tatactcgcc	cctctgagag	tgagctgtgg	720
gacatgtggg	cagggtatccg	caacaatgac	gggaaacttag	tcattgacag	tctcttacag	780
tacatcaatc	agagggaaagaa	gttcaagaagg	cgctgggttg	gagctttgc	ctctgttaact	840
atccccatcc	attttatctt	tgggcattt	gatcccttttt	atccctatcc	agagttttt	900
gagctgtaca	ggaaaacgct	gccgcggtcc	acagtg	ttctggatga	ccacattagc	960
caactatccac	agctagagga	tcccatgggc	ttcttgaatg	catatatggg	cttcatcaac	1020
tccttctgag	ctggaaagag	tagctccct	gttattaccc	ccctactccc	ttatgtgttg	1080
tgtatccac	traggaagaa	atgccccaaa	gaggctctgg	ccatcaaaca	taattcttc	1140
acaaggatcca	ctttactcaa	attgggtgaac	agtgtataagg	aagaagccag	caggagctct	1200
gactaagggtt	gacataatag	tccacccccc	attactttga	tatctgtatca	aatgtatagal	1260
cttggctttt	tttttgtgc	tattaggaaa	ttctgtatgag	cattactatt	cactgtatgca	1320
gaaagacggt	cttttgcata	aaagactttt	tttaacaccc	tggacttctc	tgaaatattt	1380
agaagtgcta	atttctggcc	cacccccaac	aggaattcta	tagtaagggg	gaggagaagg	1440
ggggctccctt	ccctcttccc	gaatgacggt	atgggcacat	gccttttaaa	agttcttaa	1500
gcaacacaga	gctgagtcct	ctttgtcata	cctttggatt	tagttttca	tcaagctgttt	1560
ttagttataa	acattttgtt	aaaatagata	ttggtttaaa	tgatagacta	ttttaggtat	1620
gattnaagac	tatgattttac	ctatacatta	tatataaaaa	ataaaagatac	taaaccagca	1680
tacccttact	ctgcccagat	agtgaagcta	attaaacacg	tttggtttct	gaataaatttg	1740
aactaaatcc	aaactatccc	ctaaaatcac	aggacattaa	ggaccaatag	catctgtgcc	1800
agagatgtac	tgttatttagc	tgggaagacc	aattctaaca	gcaaataaca	gtctgagact	1860
cctcataaccc	cagtggttag	aagcatgtct	ctttttaggt	acagtagagg	ggaagggatt	1920
gttgtgttagt	caagtccacca	tgctgaatgt	acactgattc	ctttatgatg	actgtttaac	1980
tcggccactgc	ctgtcccgaga	gaggctttcc	aatgttagctc	agtaatttcc	gttactttac	2040
agacaggaaa	gttccagaaa	ctttaagaac	aaactctgaa	agacccatga	gcaaatggtg	2100
ctgaataactt	tttttttaaa	gccacatccc	attgtttag	tcaaagcagg	attattaagt	2160
gattattttaa	aattcgtttt	ttttaattag	caacttcaag	tataacaact	ttgaaaacttg	2220
aataagtggtt	tattttctat	taataaaaaat	gaattgtgac	aaaaaaaaaa	aaaggcttcg	2280
gcttttgaag	tctatgtgt	gggggggggt				2310

## (2) INFORMATION ON SEQ ID NO. 3:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 854 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ctgcacgggg gctcgggctc actataaaag gtgggagcgc gtgggtcccc agcaacgacg 60  
 agtttcagaa cgatggagag ctcccgcgtg aggctgctgc ccctcctggg cgccgcctg 120  
 ctgctgatgc tacccctgtt gggtacccgt gcccaggagg acgcccagct ccagccccg 180  
 gcccctggaca tctactctgc cgtggatgat gcctcccacg agaaggagct gatcgaagcg 240  
 ctgcaagaag tcttgaagaa gctcaagagt aaacgttgc ccatctatga gaagaagtat 300  
 ggccaagttcc ccattgtgtga cgccgggtgag cagtgtgcag tgaggaaaagg ggcaaggatc 360  
 gggaaagctgt gtgactgtcc ccgaggaacc tccttgcatt ccttccttcctt gaagtgc 420  
 tgaaggggcg tccatttcctcc tccatatac cccatcccttc tactttcccc agaggaccac 480  
 accttcctcc ctggatgtttg gcttaagcaa cagataaaat ttatatttttcttgc 540  
 aaagggtctt ttatctgttgc ttatcaaaaat aaaagaacac attagatgtt actgtgtgaa 600  
 gaataatgcc ttgtatggtg ttgatacgtg tggatgtat tcttatttttta ttgtctgac 660  
 aaactcttgt gtacctttgt gtaaaagaagg gaagctttgt ttatcaaaaatgttgc 720  
 tggatgttgc cagaatgaaa attagatcta gctaatctcg gtagatgtca ttacaacctg 780  
 gaaaataaaat caccctaagt gacacaaatt gaagcatgtt caaaatataac ataataaaatgttgc 840  
 gtttttaataatttgc 854

## (2) INFORMATION ON SEQ ID NO. 4:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

cgcccaaaaaa gtcggggggcc cggagggggac tcggagcggg ccaagggggcg gctccggcg 60  
 gcgactcggtt agcggggccgc ggagtgaccgc ggacagctgt cctctctgac accaccccccgg 120  
 cctgcctctt tggggccatg agagctgcctt acctcttcctt gctattccctg cctgcaggct 180  
 tgctggctca gggccatgtt gacctggacc cgtctggccgc gttccctgac cacgtccagt 240  
 acacccacta tagcgaccatg atcgacaacc cagactacta tgattatcaa gaggtgactc 300  
 ctccggcccttc cgaggaacatg ttccagttcc agtcccagca gcaagtccaa caggaagtca 360  
 tcccaaaaaa aaccccaaaaaa ccagggaaatg cagagctggc gccccacagag cctggggccctc 420  
 ttgactgcccgg tgaggaacatg taccctgtca cccgcctctt ctccatatac acggccttgca 480  
 aacagtgtctt caacgggttc tgcttctaca gcctccggccg tgggttacgtc attaacaagg 540  
 agatctgtgt tggtagatgt tggcccatgtt aggagctctt cggagctgtac ctctgtcg 600  
 acaatgtggc caaaatgtggc gtatggcca gcaagccctt gtggccatacc gtggcgccct 660  
 cctgtgcccgg gggctgtggg agctgtctgg gttgggtctgg catcctgttgtt cctggccctc 720  
 ctggatctt gggccctccgg gcccctgttgtt acctgggtgtt tttttccca tccccatgtt 780  
 ccttttattt tggaaaaatgt tagtggactg cggccctggg gttggcaggc tgggtgtcc 840  
 cggcccccgg cttcagccctg tgccacccctc tggggcacga tggggggctcc ccactgccc 900  
 gtctgccccctt cgggttgggg ggtatccca gggccctctgt tggggaccctg gggccctgtacg 960  
 ggccctctca gcccgttttgg aggacacagaca gttccccggag gttaggttataca tccccccacc 1020  
 ccagctggtc tggatcttacagcc cccgtggca tggaccacct ttatttata 1080  
 caaaaaataaaaa aacaatttttt tacaataaaaaa aa 1112

(2) INFORMATION ON SEQ ID NO. 5:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1051 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

## (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

09623400-1222700

```

gcgcaggcgc gaagaagctg gcaggggcac gagccgggg cgggtttgaa gacgcgtcgt 60
tgggtttgg aggccgtgaa acagccgtt gatgttggct gccccgtggag aacgtttgtc 120
agggggcccg ccaagaagga gccccgcctg ttacgatggt gtccatgagt ttcaagcgga 180
accgcagtga cccgttctac agcaccgcgt gctgcggctg ttgcctatgtc cgacccggga 240
cgatcatcct ggggacctgg tacatggtag taaacctatt gatggcaatt ttgctgactg 300
tgaagtgac tcatccaaac tccatgccag ctgtcaacat tcaagtatgaa gtcatcggt 360
attactattc gtctgagaga atggctgata atgcctgtgt tcttttggcc gtctctgttc 420
ttatgtttat aatcagttca atgctggttt atggagcaat ttcttatcaa gtgggttggc 480
tgattccatt cttctgttac cgacttttg acttcgtcct cagttgcctg gttgcttatta 540
gttctctcac ctatggcca agaatcaaag aatatctggta tcaactacat gatttccct 600
acaaaagatga cctcctggcc ttggactcca gctgcctcct gttcattgtt cttgtgttct 660
ttgccttatt catcattttt aaggcttatac taattaactg tgtttggaaac tgctataaat 720
acatcaacaa ccgaaacgtg ccggagattt ctgtgtaccc tgcctttggaa gcaccccttc 780
agtagtttt gccaacctat gaaatggccg tgaaaaatgcc tgaaaaagaa ccaccacetc 840
cttacttacc tgcctgaaga aattctgcct ttgacaataa atcctatacc agtttttgt 900
ttgtttatgt tacagaatgc tgcaattcaag ggctttcaa acttggtag atataaaata 960
tggtggccct ttggttttaa agcaattttat ttccaaaac actaaggag ccttttggaa 1020
catctggta aacggccttt ttgggttttt t 1051

```

## (2) INFORMATION ON SEQ ID NO. 6:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1516 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

gttgtccca tccctctcat acagggtgac caggacgttc ttgagccagt cccgcattgcg 60  
 caggggaaq aagatccatg agaaggagaa gcgcctggag gcaggagacc accccgtgga 120  
 gctgtggcc cgggacttcg agaagaacta taacatgtac atcttccctg tacactggca 180  
 gttcggccca cttggaccagc accccattga cgggtacetc tccccacaccg agctggctcc 240  
 actgcgtgct cccctcatcc ccatggagca ttgcaccacc cgtttttcg agacctgtga 300  
 cctggacaat gacaagtaca tcgccttggg tgagtgggccc ggctgtttcg gcatcaagca 360  
 gaaggatatc gacaaggatc ttgtatcta aatccactcc ttccacagta cccgatctc 420  
 tcttttaaccc tcccccttcgt gtttccccca atgtttaaaa tggggatg gtttggatg 480  
 ctgcctggag acaagggtgct aacatagatt taagtgaata cattaacggt gctaaaaatg 540  
 aaaatctaa cccaaagaaca tgacattttt agctgttaact taactttaaa ggcctttcc 600  
 acacgcattt aatgtccat ttttcttttgc ccatggatg ctttgccttgc ttttgcatttgc 660  
 ggcacatggg gtggacacgg atctgttggg ctctgccttta aacacacattt gcaatggatg 720  
 cttttctttt tagtgtttcg tttgaaacta atacttaccg agtcaagactt ttttgcatttgc 780  
 tcattttcagg gtcttggctg cctgtggct tccccaggatg gcctggaggt gggcaaaagg 840  
 aagtaacaga cacacgtgt ttttgcatttgc ttttgcatttgc ttttgcatttgc 900  
 gagatccctg cagaaccacaa caccacaaac gtgggtttgc ttttgcatttgc 960  
 agattttggg gctgtttat gaaaatataa acatttcac ataaaggccaaatg ttttgcatttgc 1020  
 ttttgcatttgc ttttgcatttgc ttttgcatttgc ttttgcatttgc ttttgcatttgc 1080  
 gggagcacgg actgtcaatg ttttgcatttgc ttttgcatttgc ttttgcatttgc 1140  
 ctctgttttgc ttttgcatttgc ttttgcatttgc ttttgcatttgc ttttgcatttgc 1200  
 agccaggaag gccaaatca aqagtggatg ttttgcatttgc ttttgcatttgc ttttgcatttgc 1260  
 ttggtaatc ggttggatc ttttgcatttgc ttttgcatttgc ttttgcatttgc ttttgcatttgc 1320  
 tccttccctt ttttgcatttgc ttttgcatttgc ttttgcatttgc ttttgcatttgc ttttgcatttgc 1380  
 atggggagggg tcggatccta caggcctgag aatcggtcaa tccttccctt ttttgcatttgc 1440  
 aggcggcttc ttttgcatttgc ttttgcatttgc ttttgcatttgc ttttgcatttgc ttttgcatttgc 1500  
 tcctccaaaaataaaaaa ttttgcatttgc ttttgcatttgc ttttgcatttgc ttttgcatttgc 1560

## (2) INFORMATION ON SEQ ID NO. 7:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2367 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

cgccggggact cttggcggtt gaagggtgtgt gtcagctttt gcgtcaactcg agccctgggc 60  
 gctgctgct aaagagccga gcacgcgggt ctgtcatcat gtcgcgttac gggcggtacg 120  
 gaggagaaac caaggtgtat gttggtaacc tgggaactgg cgctggcaaa ggagagtag 180  
 aaaggcctt cagttattat ggtcccttaa qaactgtatg gattgcgaga aatccctcag 240  
 gatggcctt tggaaattt gaagatccta gagatgcaga agatgcagta cgaggactgg 300  
 atggaaaggat gatggcggc tcccgagtga ggggtgaact atcgacaggc atgcctcgga 360  
 gatcacgtt tgatagacca cctgccccac gtccctttaa tccaaatgtat gatgtatgg 420  
 agtgtggcga aaaggacat tatgtttatg attgtcatcg ttacagccgg cgaagaagaa 480  
 gcagggtcag qtctagatca cattctcgat ccagaggaag ggcataactct cgctcacgca 540  
 gcaggaggcag gggacgaagg tcaaggtcag catctcctcg acgatcaaga tctatctctc 600  
 tccgttagatc aagatcagct tcactcagaa gatcttaggtc tggttctata aaaggatcga 660  
 ggtatttcca atccccgtcg aggtcaagat caagatccag gtctatttca cgaccaagaa 720  
 gcagccgatc aaagtccaga tctccatctc caaaaagaag tgcgtcccca tcaggaagtc 780  
 ctcgcagaag tgcaagtctt gaaagaatgg actgaagctc tcaagttcac ccttttaggga 840  
 aaagttatccat ttgttacatt attataaggg atttgtgtat tctgtaaagt gtaaccttagg 900  
 aaagataatt caaccatcta atcaaaaatgg atctggatta ctatgtaaat tcacagcagt 960  
 aagataataat aaattttgtt gaatgttata acatcatatg gtctgaaaat gtgggttttt 1020  
 atttggcaca tttaaataaa atgttctaa ctgattttt gatttgtgtt caatattaac 1080  
 acttcttaat ttgatataatt tgagagtca gacattataat tggtaacctt attcatacat 1140  
 acctacattc aqaattgaaa ggtgttgggtt aagtcttggaa catcaactatt ctatgcataa 1200  
 aacttggcca gnatcttaag ggactttgaa aattccatct tacccttgcgta gctctgggt 1260  
 agatgacctg agtcccttat gatacagcct gaatgcatac tgacagatcc ttaagtttagc 1320  
 taatccgttt gaagttgggt ttagtaggtt ttgtatgatc agtgggtgaag caagtaggac 1380  
 cactgatgtg tctaaatgag catgacagga actaaacgaa actgattaaa tggatgaga 1440  
 atagaaactg atttctggat gatcttata ctaattgcag ctggcaggct actagggtggc 1500  
 atagtgttaa ttaggactcc ccaagatatg gggagttctt ctctcaatgg tcttgggtct 1560  
 ttgctttcta cattagttaa ccagttttat accaaaaaaat gcatgtttga ggaattgtct 1620  
 gaaattggga caaaacacct tcatgtaaac cagcttgcgaa aatcttcca gcccagatac 1680  
 tcttcatcta ttcaaatggg ttgtcttatt ctgagcaaaag acctgttggtt aatcttcaag 1740  
 cttaggttttgcagttcccaa ccacaacatt ctctatctt gcaaggctgg tgcaagtaa 1800  
 ttaaagatgt caatcagaaa tgtcaatgag actaaagtgg tttgttaaat ctcagctata 1860  
 tttagcaaca ctccatgtat ctaatatttt ttggtagcat ctggtagacc ttagaatgtt 1920  
 acatagccag taggttctttt attcaaaattt taagttatctt aagaatagta gggcagtaac 1980  
 agttactttt gagagttttc tggtcaagct ttaccaggc attctcttagc ctgggtacaa 2040  
 aaaaaaaaaa aacctgctgg ttgcgcagat acctaggctt gtccatttttgcattttcag 2100  
 caaagtcatgg qgatactatt gcaactggg aatactggc tgcatcaagt tatttcggta 2160  
 gtttgaccgc tagtatgttg gaagttattt ggattgtttt tggaatttttgcactggctgaa 2220  
 ttatgggtgg tataaaagtttca tggtataac tggcaggctt atttatctgt tgcacttggt 2280  
 tagcttaat tggtctgtat tattttaaaga taagttact caacaataaa tctgcagaga 2340  
 ttgaacaaat aaaaaaaaaa aaaaaaaaaa 2367

(2) INFORMATION ON SEQ ID NO. 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

ctcgagccgt ggccagtgcc cgcgaatgcg cggagacact gacccatcgc gcctcggtc 60
cagcgccatg ggcgcctcca ggaagttctt cgttggggga aacttggaaaga tgaacggggcg 120
gaagcagagt ctggggggagc tcattggcac tcttgaacgcg gccaagggtgc cggccgacac 180
cgaggtggtt tgggtctcccc ctactggcta tatcgacttc gccccggcaga agcttagatcc 240
caagattgtt gttggctgcgc agaactgtctt caaaagtgtact aatggggctt ttactgggaa 300
gttcggccct ggcatgtatca aagactgtcg gaccacgtgg gtggctctgg ggcactcaga 360
gagaaggcat gtctttgggg agtcagatgtt gctgtttttttt cagaaaatgtgg cccatgtctt 420
ggcagagggaa ctgggatgtttt tcggctgtcat tggggagaaag ctagatgtaaa gggaaatgtgg 480
catcaactgtttt aatgtttttt tcggatgtttt aaaaatgtttt gggggatgtact tgaaggactgtgg 540
gttcggccctt gttggctt

```

568

(2) INFORMATION ON SEQ ID NO. 9:

**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1775 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

## (C) ORGAN:

## (vii) OTHER ORIGIN:

## (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ctcggggggcc atttttgtgaa gagacgaaaga ctgagcgggt tgccgcgt tgccgaccc 60  
 cagcagcagt cggcttctct acgcagaacc cgggagtaagg agactcagaa tcgaatctct 120  
 tctccctccc ctctttgtga gattttttgc atcttcagct acattttcgg ctttgcgaga 180  
 aaccttacca tcaaaccacga tggccagcaa cgttaccaac aagacagatc ctcgctccat 240  
 gaactcccggt gtattcattt ggaatctcaa cactcttgcgt gtcaagaaat ctgtatgttga 300  
 ggcatacttt tcgaagatgt gcaaattgtt gggctgtctt gttcataagg gctttgcctt 360  
 cgttcagtat gtaatgaga gaaatgcccgg gctgtgtat gcaggagagg atggcagaat 420  
 gattgtctggc cagggttttag atattaacctt gctgtcagag ccaaaagtga accgaggaaa 480  
 agcagggtgtg aaacgatctg cagcggagat gtacggctcc tcttttgcgt tggactatga 540  
 ctttcaacgg gactattatg ataggatgtt cagttaccca gcacgtgtac ctccctcc 600  
 tcctattgtt cgggctgttag tgccctcgaa acgtcagcgt gtatcaggaa acacttcacg 660  
 aaggggcaaa agtggcttca attctaagag tggacagcgg ggtatcttca agtctggaaa 720  
 gttgaaagga gatgacccattaa agggagctg acccagataa aacaaaaaagt 780  
 ggattctctc ctggaaaacc tggaaaaat tggaaaaggaa cagagcaaac aagcagttaga 840  
 gatgaagaat gataagtca gaaaggagca gagcagcagc tccgtgaaga aagatgagac 900  
 taatgtgaag atggagtctg aggggggtgc agatgactct gctgaggagg gggacctact 960  
 ggatgatgtat gataatgaaat atcggggggta tgaccagctg gagttgatca aggatgatgat 1020  
 aaaagaggct gaggaaaggag aggtgacag agacagcgc aatggcgagg atgactctt 1080  
 agcacatagt ggggtttttaga aatcttaccc cattattttt ttaccttaggc gcttgcataa 1140  
 gatcaaattt ttacccatg cctctccctt agtacccatc gcacatgctc actgttctcc 1200  
 ccatecttgt cttcccttcatg ttcatattt catattgcgc cgcccttagt cccatttca 1260  
 cttcccttga cgtcccttagt agttttgtta agtcttaccc tgtaatttt gcttttatt 1320  
 ttgataacctc ttatgactt aacaataaaa aggtgtatg gttttatca actgttctcc 1380  
 aaataatctc ttgttatgca gggagttacag ttcttttcat tcatacataa gttcagtagt 1440  
 tgcttcccta actgcaaaagg caatctcatt tagttgagta gctcttgaaa gcagcttgc 1500  
 gttagaagta tgggtgttac accctcacat tagtgtgtt gttggggcag ttcaacaca 1560  
 atgtacaat gtatgtttt gatgtgaggt tggcatgtca aatgcacccct ctagaaaaat 1620  
 aatttagtgtt atagttttt gatgtttt ctaaagtgtt tactgtgggt tatttttg 1680  
 aacagccctga tgggtggac cttttttccct caaaataaaac aagtcccttat taaaccagg 1740  
 atttggagaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1775

## (2) INFORMATION ON SEQ ID NO. 10:

## (i) SEQUENCE CHARACTERISTIC:

---

(A) LENGTH: 509 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

caaggctcgagt ggccactcgcg cagaccagac ttgcgtcgta ctgcgtgcgccc tcgcttcgct 60  
tttccctccgc aaccatgtct gacaaacccg atatggctga gatcgagaaa ttgcataaagt120  
cgaaaactgaa gaagacagag acgcaagaga aaaatccact gccttcgaaa gaaacgattg180  
  
aacaggagaaa gcaaggcaggc gaatcgtaat gagggcgtgcg ccgc当地at gcactgtaca240  
ttccacaagc attgc当地tct tatttactt ct当地tagctg tt当地actt当地 taagatgcaa300  
agaggttggta tcaagttaa atgactgtgc tgcccccttc acatcaaagg gactacttga360  
acaacggaaag gggcgcggcc taccttcccc atctgtctat ctatctggct ggc当地ggaaag420  
ggaagagtttg caaggcttggta aggaagaagt ggggttggaaag aagttggatg ggccgcccagt480  
aaaacttqqq taaaccgaaac ttggccaaag 509

(2) INFORMATION ON SEQ ID NO. 11:

(i) SEQUENCE CHARACTERISTIC

- (A) LENGTH: 2191 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

actgagcggag	ggccagccgt	gcggcatctta	caccgagcgc	tgtggctccg	gccttcgctg	60
ccagccgtcg	cccgacgagg	cgcgaccgct	gcagggcgctg	ctggacggcc	gcgggctctg	120
cgtcaacgct	agtgccgtca	gcccgcctgcg	cgccctacctg	ctgcccagcgc	cgccagctcc	180
aggaaatgct	agtgagtccgg	aggaagaccg	cagcgccggc	agtgtggaga	gcccgtccgt	240
ctccagcacg	caccgggtgt	ctgatcccaa	gttccacccc	ctccatcaa	agataatcat	300
catcaagaaa	gggcgtctaa	aagacagcca	gcccgtacaaa	gttgcatacg	agtctcagag	360
cacagatacc	cagaacttct	cctccgagtc	caagcgggag	acagaatatg	gtccctggcg	420
tagagaaatg	gaagacacac	tgaatcacct	gaagttccctc	aatgtgctga	gtcccaagggg	480
tgtacacatt	cccaactgtg	acaagaaggg	attttataag	aaaaaagcagt	gtcgcccttc	540
caaaggcagg	aagcggggct	tctgctgggt	tgtggataag	tatgggcagc	ctctcccaagg	600
ctacaccacc	aaggggaaagg	aggacgtgca	ctgctacagc	atgcagagca	atgcagacgcc	660
tgccgcaagg	ttaatgtgga	gctcaaatat	gccttatttt	gcacaaaaga	ctgccaagga	720
catgaccacgc	agctggctac	agcctcgatt	tatatttctg	tttgggtgtga	actgattttt	780
tttaaaccaa	agtttagaaa	gagggttttg	aatgcctat	ggtttttttt	aatggtaaac	840
ttgagcatct	tttcaactttc	cagtagtcag	caaagagcag	tttgaatttt	cttgcgcgtt	900
cctatcaaaa	tattcagaga	ctcgagcaca	gcacccagac	ttcatgcqcc	ctgtggatgtc	960
tcaccacatg	ttggtcgaag	cgggcgacca	ctgactttgt	gacttagggt	gtctgtgttgc	1020
ctatgttagag	aacacgttcc	acccccactc	cccgtagact	gcccacacggc	tttatcgagat	1080
ataggaaaac	ctttaaacc	cggtcatccg	gacatcccaa	cgcatgc	tggagctcacl	1140
agccttctgt	ggtgtcattt	ctgaaaacaag	ggcgtggatc	cctcaaccaa	gaagaatgtt	1200
tatgtcttca	agtgcacctgt	actgcttggg	gactatttgg	aaaaataagg	tggagtcctt	1260
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tccacattca	gaggcatcac	aagtaatggc	acaatttttc	ggatgactgc	agaaaatagt	1500
gttttgcgt	tcaacaactc	aagacgaagc	ttatccctgt	ggataagctc	ttttaaggca	1560
aagctttatt	ttcatctctc	atcttttgc	ctccttagca	caatgtaaaa	aagaatagt	1620
atatcagaac	aggaaggagg	aatggcttgc	tggggagccc	atccaggaca	ctgggagcac	1680
atagagattc	accatgttt	gttgcactta	gagtcatct	catgttttc	tttataattc	1740
acacatata	gcagagaaga	tatgtcttgc	ttaacattgt	atacaacata	gccccaaata	1800
tagtaagatc	tatactagat	aatccttagat	gaaatgttag	agatgtata	tgatacaact	1860
gtggccatga	ctgaggaaag	gagctcacgc	ccagagactg	ggctgtctc	ccggaggccca	1920
aacccaagaa	ggtctggcaa	agtcaaggctc	agggagactc	tgccctgt	cagacctcg	1980
tgtggacaca	cgctgcata	agctcttctt	gaaaacagag	gggtctcaag	acattctg	2040
taccttattag	cttttcttta	tttttttaac	tttttgggg	gaaaagtatt	tttgagaagt	2100
ttgtcttgc	atgtattttat	aaatagtaaa	raaagtttt	accattaaaa	aaaaaaggag	2160
taaaaaa	aaaaaggccg	gcccgcqact	a			2191

## (2) INFORMATION ON SEQ ID NO. 12:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1769 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

attatttaca tttcaaaata attcccccta atcgaaaaac tccttaagttc attaccattg 60  
 ttggccacc tttaggttcca ccacccgtt gttaccccaag ccctgggttc aaacaggac 120  
 atggcaaggg gacacaggac agaggggtcc ccagctgcca cctcacccac cgcaattcat 180  
 tttagtagcag gcacaggggc agctccggca cggcttctc aggcctatgc cggagcctcg 240  
 agggctggag agcggaaaga caggcagtgc tcggggagtt gcaagcaggac gtcaccacca 300  
 gggcgaacgg ccacgggagg gggggcccccgg gacattgcgc agcaaggagg ctgcaggggc 360  
 tcggcctgcg ggcggccggc ccacaggac ctgcggccca gggctctggg cggagagggc 420  
 ccacagtggc ctgggtgacg ctgtatgccc tcaccgctca gcccctgggg ctggcttggc 480  
 agacagtaca gcatccaggc gagtcaaggc catggggcga gaccagacta ggcgaggcgg 540  
 gcggggcggc gtgaatgagc tctcaggagg gaggatggtg caggcaggagg tgaggagcgc 600  
 agggggcggc gaggcggagg cactggcctc cagagccgt ggcacaaggc ggcctcgcgg 660  
 gcgccgacgg agccgggatc ggtgcctca ggttcgggct gtagacgagg ccaggctctcc 720  
 agctgggtg gacgtgccccca ccagctgccc aaggcaagac gccaggcccg gtggacgtga 780  
 caagcaggac atgacatggc cgggtgtgac qgcgaggaca gaggaggcgc gtcggccctt 840  
 cctgaacacc tttaggctggt ggggctgcgg caagaagcgg gtctgtttt ttacttccctc 900  
 cacggagtgc gcacactatg gctgcccctt gggctcccag aaccacaaac atgaaagaaa 960  
 tggtgctacc cagctcaagc ctggggccctt gaatccggac aaaaaaccctt cttagttggal020  
 aatgaatatg ctgtacttta caaccactgc actaaetgac ttaggaaatcg gtcggaaagl080  
 gtgaaqctag aggaaccaga cctcatcaac ccaacatcaa aqacaccatc ggaacagcagl140  
 cgcccgacgc acccaccctt caccggcgcac tccatcttca tggccaccccc ctqcgccggal200  
 cggttgacca ccagccacca catcatccca gagctgagct cctccagcgg gatqacgcccgl260  
 tccccaccac ctcccccttca ttcttttca tccttctgtc tctttgttcc tgagctttccl320  
 tgcctttctt ttccctgtgg agattcaaaag cctccacgcac tctgtttccccc ccgtcccttc1380  
 tgaatttaat ttgcactaaag tcatttgcac tggttggagt tggagacgc gctttagtgc1440  
 tcagtacgag tgcgtgtgag tgcgtgaccac ctggcaagt gctgtgcac ggcggcccg1500  
 ccctccatct gggccgggtg actggggcgc ggcgtgtgtc ccggaggccctc accctgccc1560  
 cgccctatct ggaagctccg accgacatca cggagcagcc ttcaagcatt ccattacgccc1620  
 ccatctcgct ctgtgccccctt cccaccagg gcttcagcag gaggccctggg ctcatcatca1680  
 ataaaactg ttacagcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa1740  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaag

1769

(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC

- (A) LENGTH: 1026 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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aaaagctgtc cgccgcgggaa gccccagggcc agctttgggg ttgtccctgg acttgttttg 60
gttccagaac ctgacgaccc ggcgacggcg acgtctctt tgactaaaag acagtgttcca 120
gtgctccagc cttaggagtct acggggaccg cttcccgccg cggcaccatg cccaaactct 180
ctggcaactg gaaaatcatc cgatcgaaaa acttcgagaga attgtctaaa gtgctggggg 240
tgaatgtgat gctgaggaag attgtctgtgg ctgcagcgtc caagccagca gtggagatca 300
aacaggaggg agacactttc tacatcaaaa cttccaccac cgtgcgcacc acagagatta 360
acttcaaggt tggggaggag tttgaggagc agactgtgga tgggaggccc tctaagagcc 420
tggtaaatg ggagagtgag aataaaatgg tctgtgagca gaagctctg aaggggagagg 480
gcccccaagac ctcgtggacc agagaactga ccaacgtgg ggaactgtac ctgaccatga 540
cgccggatga cgttgtgtgc accaggggtct acgtccgaga gtgagtgccc acaggtagaa 600
ccgcggccga agccccaccac tggccatgtt caccggccctg cttcaactgccc cccctccgtcc 660
cacccccctcc ttcttaggata ggcgtccccctt taccggcgtc actttctgggg gtcaactggg 720
tgcctcttgc agggtcttgc tttcttgc acgtttcttc ctccccctaca ccaacacaaga 780
ggaatggctg caaagagccca gatcaccat tccgggttca ctccccggct ccccaagtca 840
gcagtcctag ccccaaaccac gccccagagca gggtctctt aaaggggact tgagggcctg 900
agcaggaaaag actggccctc tagcttctac ctttgcctt tgcgtat acagttttaga 960
atatttatgtt gttatgttta taaaatgtt taaaaaaaat aaaaaaaaaa aaaaaaaaaaa 1020
aaaaaaaaa 1026

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(2) INFORMATION ON SEQ ID NO. 14:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 676 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ggccattttg tgaagagacg aagactgagc ggttgtggcc gcgttgccga cctccagcag 60  
 cagtcggctt ctctacgcag aacccggag taggagactc agaatcgaat ctcttctccc120  
 tcccccttctt gggcagcaag gcgaaaccca tccctactca ctggagctca gctttgat180  
 ttaacctccc ttccccaccc ttccagaaca cacacattcc attccaaaac tgattttata240  
 aagacatttt aaacataatg atgcaacttg gtgtgcacta cagcaaatgt acaggtgtt300  
 ttttttaat tgtttccaaa accgggacct ggatttaaga tptaattttt aaaatttcta360  
 tttctatttt ttcggcagca gttgggttag aggaggagga gccttttagc ctcccagaaa420  
 ctgacctctc tacttctcg tgtatttta agattgattg atgatgtgga aagggtttg480  
 ctgtctgtct actgaaaact ttatccttgc ggttttgtg gaactgcgtt tggaaaqaga540  
 aaagaaaatga accttactga cttgacattt tgcacccccc ggttttcgaa tctgggcaat600  
 ttaattttg gttttacagt gagagttttt gatctcagca cagaagtaat ccaattttt660  
 tttagcatttt ccgact 676

(2) INFORMATION ON SEQ ID NO. 15:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1254 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

cggttcggcc  agtcgtggcg  gctcaaacac  ctcatttgac  cttgccagct  gacccctaaa  60
ccctgcattt  gaaccgacca  acattaagtc  cagagagtaa  acttgaatgg  aataacgaca  120
ttccagaagt  taatcatttg  aattctgaac  actggagaaa  aaccgaaaaa  tggacggggc  180
atgaagagac  taatcatctg  gaaaccgatt  tcagtgccga  tggcatgaca  gagctagagc  240
tcggggcccag  ccccaggctg  cagccccattc  gcagggcaccc  gaaagaactt  ccccagtatg  300
gtggtcctgg  aaaggacatt  tttgaagatc  aactatatct  tcctgtgcat  tccgatgaa  360
tttcagttca  tcagatgttc  accatggcca  cccgcagaaca  ccgaagtaat  tccagcatag  420
cggggaaagat  gttgaccaag  gtggagaaga  atcacgaaaa  ggagaagtca  cagcacctag  480
aaggcagcgc  ctccctttca  ctctcccttg  attagatgaa  actgttacct  taccctaaac  540
acagtatttc  ttttaactt  ttttattttgt  aaactaataa  aggttaatcac  agccaccaac  600
attccaagct  accctgggt  cccctgtgca  gtagaagcta  gtgagcatgt  gagcaagcgg  660
tgtgcacacg  gagactcatc  gttataattt  actatctgcc  aagagttagaa  agaaaggctg  720
gggatatttg  ggttggctt  gttttgattt  ttgttgcattt  tgttttgtttt  gtactaaaac  780
agtattttct  ttgtatatac  gttagggacat  aagtatatac  atgttatacca  atcaagatgg  840
ctagaatgg  gcctttctga  gtgtctaaaa  ctgtacaccc  ctggtaatcc  ttcaacacaca  900
cttccactgc  ctgcgtaatg  aagttttgat  tcatttttaa  ccacttggaaat  ttcaatgc  960
cgtcattttc  agtttagatga  ttttgcactt  tgagattaaa  atgccatgtc  tattttgattt  1020
gtcttatttt  ttatttttta  caggcttattc  agtcttactg  ttggctgtca  ttgtgacaaa  1080
gtcaaataaa  cccccaagga  cgacacacag  tatggatcac  atattttttg  acattaaagct  1140
tttgcctggaa  aatgttgcatt  gtgttttacc  tcgacttgc  aaaatcgatt  agcagaaaagg  1200
catggcttaat  aatgttggtg  gtggaaaataa  ataaataagt  aaacaaaaag  aaaa  1254

```

(2) INFORMATION ON SEQ ID NO. 16:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 537 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

**(vi) ORIGIN:**

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ggcccgggccc cccaccctcg acatgcgcgtt ccggcgacgc cttagcgctg acccccacgc 60  
 aaccaggcga aactccgcgg aggcgcgcgg cacgatggac ggtcggtgc agctgatgaa120  
 ggccttcctg gccggggcccc tccggcccgcc ggcgcgtcgc tggaggaacc cgattccctt180  
 tcccgagacg ttgcacggag atacccgaccg actcccgag ttcatcggtgc agacgtgctc240  
 ctacatgttc gtggacgaga acacgttctc caacgacgac ctgaagggtga cgttccat300  
 cacccgcctc acggggccag ccctgcagtg ggtgatcccc tacatcagga aggagagccc360  
 cctgtcaat gattacggg gcttctggc cgagatgaag cgagtcttg gatgggagga420  
 ggacgaggac ttcttagggc ggagaccctc gggcctgggg gcgggtgc tggaaagagt480  
 tcgtgtgcc agtggccacc gcttagggctc ccacaggcgc cttccccagg gaatgt 537

## (2) INFORMATION ON SEQ ID NO. 17:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 823 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

tagactgaac aggaggggga gtcctgggta gcgcgccggc ctaaatcggtt acttggcgga 60  
aagtcccat gactcttgc cagcgcccccc ctccctttgt gaggatggg atatccgac120  
 tccttaaggc cctggcgac ataaagggtgtt accttttcat tcccgttggt atggagggcc180  
 acatctgcga gaggcctggag tctgcgaagg ccgggaccgg gttcccccggc ccacagtggg240  
 ggtgtgcaaa cccgagagaa ctgggttgca aattcgtgaa gaaatcagcat catgtttggc300  
 agctgagttt tggagccagg agcctgcccattt gagggtttgtt gaaacagagtg ctgttttaga360  
 gctggcagca gcatctcagc ccaagagaag gttatattcc cagaggatgt cagttccaaag420  
 gaccagtgc tgccatcagt ttggattctg aaaactaact ggcatcaaca ctgggtgttag480  
 aaacatgtt gccttatgtt tcaagaggaca tgctcagcag atccaagaga tatatttggc540  
 aactttttttt agaaaaggca cattgggtat cattcattac atttttgagg ttttttttggg600  
 tttttttttt ttttttttga gacagtcttg ctgtattggc caggctggga gtgtgggtggc660  
 acaatcacag ctcatcgat cctcaatcac ccaggcccta agcaatccctc ccacccgtt720  
 gctgggacta cagctcacag cacaccgggc taaaattttt tttttgtttagt acggttttt780  
 tatgttgccc ggggtggttt caggggtccgg ggttcagatg gtc 823

## (2) INFORMATION ON SEQ ID NO. 18:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

gggcgcacat aagggtgtgac cttttcattc ccgttgttat ggagggccac atctgccaga 60  
 gcctggagtc tgcgaaggcc gggacccggc tccccggccc acagtggggg tggctcaaacc 120  
 cgagagaact ggctcgctgaa acctctacaa ctttagttgac cgtaactgccc aqagccctgc 180  
 cctgaattcc tggctcttact ccctctttaa gattgcgtac ccactgcaga gtgctgaaga 240  
 cggggtagcc acgagggttgc aaattcgtga agaatacagca tcatgtttgg cagctgagta 300  
 ttggagccag gaggcctgcca tgagggttttgg agaacaagagt gctgttttag agctggcagc 360  
 agcatctca gccaagagaaa ggttatattc ccagaggatg tcagttcccaa ggaccagtag 420  
 ctggccatca gttggattct gaaaactaac tggcatcaac actgggtgtt gaaacatgtt 480  
 tgccttatgt atcagaggac atgcctcagca gatccaagag atatattttgg caactttttc 540  
 tagaaaaggc acattgggta tcattcatta cattttttagg tttttttggg tttttttttt 600  
 ttttttttgg aacatgttttgc ctgtattgcc caggctggag tgggtggca caatcacagc 660  
 tcattgcattt ctcaatcacc caggcctaag caatccccc accttggtagc tgggactaca 720  
 gctcacagca cacctggcta aaattttttt tttgttgaga cggattctct atgttgcucca 780  
 ggctggtctc aggctccctgg gctcagatgg tcctccctgcc tcaagttccca aaggcacagg 840  
 ccaagtggta gctttgtccc ttgccatcat gcccaacaag aggttctata ccttttaatg 900  
 aattgacttt cattaaattgg ttatgttggt gggcaagtcc tttaaqctgg aaattgtaaa 960  
 ttccctcctga aatgtttttt catgcagttt ccatgaacta atactacaat aaaggatgg 1020  
 ttgggggtgtt aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1080  
 aa

1082

## (2) INFORMATION ON SEQ ID NO. 19:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ccccatccat	agggaaatgag	ctggggctgtc	ctttctcccc	acgttcaccc	gcacttcgtt	60
agagagcagt	gttcacatgc	cacaccacaa	gatccccaca	atgacataac	tccattcaga	120
gactggcgtg	actgggctgg	gtctccccac	cccccccttc	agcttctgtt	tcactcagaa	180
tctggcagcc	agttccgtcc	tgacagagtt	cacagcatat	attgtgttat	tcttgcctat	240
agtgcatctg	ctttaagaat	taacgaaagc	agtgtcaaga	cagtaaggat	tcaaaccatt	300
tgccaaaaat	gagtcttaagt	gcatttactc	tcttcctggc	attgattggt	ggtaccagtg	360
gccagttacta	tgattatgtat	tttcccttat	caatttatgg	gcaatcatca	ccaaactgtg	420
caccagaatg	taactgccc	gaaagctacc	caagtgcct	gtactgttat	gagctgaaat	480
tgaaaagtgt	accaatggtg	ccttcctggaa	tcaaggatct	ttacctttagg	aataaccaga	540
ttgaccatata	tgtgaaaag	gcctttgaga	atgttaactga	tctgcagtgg	ctcattctag	600
atcacaaccc	tctgaaaac	tccaagataa	aagggagagt	tttctctaaa	ttgaaaacaac	660
tgaagaagct	gcataataaac	cacaacaacc	tgacagagtc	tgtgggccc	cttcccaat	720
ctctggagga	tctgcagctt	actcataaca	agatcacaaa	gctgggctct	tttgaaggat	780
tggtaaacct	gacccatc	catctccagc	acaatcggt	gaaagaggat	gctgtttcag	840
ctgcttttaa	aggctttaaa	tcactcgaat	accttgactt	gagcttcaat	cagatagcc	900
gactgccttc	tggctccct	gtctctttc	taactctcta	cttagacaac	aataagatca	960
gcaacatccc	tgtatgaggat	ttcaagcgtt	ttaatgcatt	gcagtatctg	cgttatctc	1020
acaacgaact	ggctgtatgt	ggaataacctg	gaaattctt	caatgtgtca	tccctgggt	1080
agctggatct	gtccctataac	aagctaaaa	acataccaac	tgtcaatgaa	aaccttggaa	1140
actattaccc	ggaggtcaat	caacttgaga	agtttgacat	aaagagcttc	tgcaagatcc	1200
tggggccatt	atccatctcc	aagatcaagc	atttgcgtt	ggatggcaat	cgcattctcag	1260
aaaccaggct	tccaccggat	atgtatgaat	gtctacgtgt	tgctaacgaa	gtcactctt	1320
attaatatct	gtatcctgga	acaatatcc	atggttatgt	ttttctgtgt	gtcagtttcc	1380
atagtatcca	tattttatta	ctgttattta	cttccatgaa	ttttaaaatc	tgaggaaat	1440
gttttgtaaa	catttatttt	tttttaaagg	aaaaggatgg	aaaggccagg	gcctaaattc	1500
catccaccaa	ggaacacaccc	acattattcc	acggaaatagg	ccatcggg		1548

(2) INFORMATION ON SEQ ID NO. 20:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 844 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

acctgcagag gggccatac ggcgttggtc tggattcccg tcgttaactta aaggaaaatt 60  
 ttcacaatgt ccggagccct tggatgtccctg caaatqaagg aggaggatgt ccttaagttc120  
 cttgcagcag gaacccactt aggtggcacc aatcttgcact tccagatgga acagracatc180  
 tataaaaagga aaagtgtatgg cacttatatac ataaaatctca agaggacctg ggagaagctt240  
 ctgctggcag ctctgtcaat tggatgtccctt gaaaacccctg ctgtatgtcaag tggatgtatcc300  
 tccaggaata ctggccagag ggctgtgctg aagtttgctg ctgcccacttg agccactcca360  
 attgtctggcc gcttcactcc tggAACCTTC actaaccaga tccaggcagc cttccgggag420  
 ccacggcttc ttgtggttac tgaccccagg gctgaccacc agcctctcac ggaggcatct480  
 tatgttaacc tacctaccat tgcgtgtgt aacacagatt ctccctctgcg ctatgtggac540  
 attgtcaatcc catgcaacaa caaggtaatg attttaggat cttagatgtt tgaatgcgtg600  
 ctctagaaaa aacattccctg tgcacattgt tagagttgg agttggggct actgactggc660  
 cgatgaactc gcaagtgttag gtatgtgtgt acatgagggg caagtttcg ctaacaccac720  
 aagggtctct ggcccaatga gtggagtttg atagtaattc ttgctacaag tataacatta780  
 ctgcatacaca gctttgtgga gaaatgaaaa catttggaaa atatgtgttt ctctgccttg840  
 tcca 844

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 862 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

gagcaagaga gaaggaggcc cagacagtga gggcaaggagg gagagaaggag acgcagaagg 60  
 agagcagcg agagagaaag gttctggat tgggggggag agcaagggag ggaggaaggc120  
 ggtgagagag gcggggggct cgggagggtg aaagggggga ggagaaggc gggcacggal80  
 ggcggcggcg agggacaaga ctccgactcc agctctgact ttttcgcgg ctctcggtt240  
 ccactgcgc catgtcactc ctcttgcgg tggctcagc cttcacatc ctcatctta300  
 tactgtttt cgtggccact ttggacaagt cctggtgac tctccctggg aaagagtccc360  
 tgaatctctg gtacgactgc acgtggaaaca acgacaccaa aacatggcc tgcagtaatg420  
 tcagcgagaa tggctggctg aaggcggtgc aggtctctcat ggtgtctcc ctcatctct480  
 gctgtctctc ttcatctctg ttcatgttcc agctctacac catgcgacqa ggaggctct540  
 tctatgccac cggccctctgc cagcttgc a cagcttgc ccagcgtggc ggtgtttact ggcccttga600  
  
 tctatgccat tcacgcccgaq gagatcttgg agaagcaccc gcgagggggc agcttcggat660  
 actgttcgc cctggcttgg gtggccttcc ccctcgccct ggtcagcggc atcatctaca720  
 tccacctacg gaagcgggag tggcgcccc gctcgctcg gctgccccccg ccccttcccg780  
 gccccccctcg ccgcgcgtcc tccaaaaaaat aaaaccttaa ccgcggggaa aaaaaaaaaa840  
 aaaaaaggaag gaaaaaaaaa aa 862

09623400 - 1222700

## (2) INFORMATION ON SEQ ID NO. 22:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 546 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

cccagccaaag ggtcccttcaq gttaggaggcc ctgggtgact ttggaaagtcc gtatgttcc 60  
 attcgcagata attttttagct tagggccctgg tggcttaggtc ggttctctcc tttccagtcg120  
 gagacctctg cccaaacat gctccgcacag atcatcggtc aaggccaaagaa gcatccgagc180  
 ttatcccccc tctttgtatt tatttggaaact ggagctactg gaccaacact gtatctttg240  
 cgtctggcat tggcaatcc agatgtttgt tgggacagaa ataaccacaa gcccggaaac300  
 aaactgggtc ccaatgttca atacaagtcc tactcagtga atgtggatca cagcaagctg360  
 aagaaggaac gtccagatcc taaatgaaa tggttcaacta taacgctgct ttagaatgaa420  
 ggtcttccaa aagccacatc cgcacaatcc tccacttaac caggaaatat ttctcctttt480  
 aatgaatga aatcaatggt ggggggcgtt attggaaagcc ctattgggt tcaagtgttg540  
 aataaa 546

(2) INFORMATION ON SEQ ID NO. 23:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1591 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ggccgaggagc	cgagccccgcc	accggggggcgc	ccggccggcgc	ccggccatggg	ctggcctcggg	60
aacagtaaga	ccgaggacca	gcgcaacgag	gagaaggcgc	agggtgaggcc	aacaaaaaaga	120
tcgagaagca	gctgcagaag	gacaagcagg	tctaccggc	cacgcaccgc	ctgctgctgc	180
tgggtgtgg	agaatctgg	aaaagcacca	ttgtqaagca	gatgaggatc	ctgcatgtta	240
atgggtttaa	tggagacagt	gagaaggcaa	ccaaagtgc	ggacatcaaa	aacaacctga	300
aagaggcgat	tgaaaaccatt	gtggccgcca	tgagcaaccc	ggtgtcccccc	gtggagctgg	360
ccaaccggaa	gaaccaggcc	agagtggact	acattctgag	tgtgatqaac	gtgcctgact	420
ttgacttccc	tcccgaaattc	tatgagcatg	ccaggcctct	gtgggaggat	gaaggagtg	480
gtgcctgcta	cgaacgctcc	aacgagttacc	agctgattga	ctgtgcccag	tacttccctgg	540
acaagatcga	cgtgatcaag	caggctgact	atgtgccgag	cgatcaggac	ctgcttcgct	600
gccgtgtccct	gacttctgg	atctttgaga	ccaaagtccca	ggtgacaaa	gtcaacttcc	660
acatgttga	cgtgggtggc	cagcgcgtatg	aacgcccaca	gtggatccag	tgcttcaacg	720
atgtgactgc	catcatcttc	gtgggtggcca	gcagcagcta	caacatggtc	atccgggagg	780
acaaccagac	caaccgcctg	caggaggctc	tgaaccttct	caagagcatc	tggaacaaca	840
gatggctgct	caccatctct	gtgatccctgt	tcctcaacaa	gcaagatctg	ctcgctgaga	900
aagtccctgc	tggggaaatcg	aagattgagg	actactttcc	agaatttgct	cgctacacta	960
ctccctgagga	tgctactccc	gagccccggag	aggaccacg	ctgtgaccggg	gccaaaggactt	1020
tcatccgaga	tgagtttctg	aggatcagca	ctgcccagtgg	agatggggct	cactactgtct	1080
accctcattt	cacctgcgt	gtggacactg	agaacatccg	ccgtgtgttc	aacgactgccc	1140
gtgacatcat	tcaacgcgt	cacccctcg	agtacgagct	gtctcaagaa	gggaaccccc	1200
aaatttaatt	aaaggcttaa	gcacaattaa	ttaaaaagtga	aacgtatgg	tacaaggcagt	1260
taatcaccca	ccatagggca	tgattaacaa	agcaacctt	ccctttcccc	gagtgtat	1320
gcgaaacccc	cttttccctt	cagcttgctt	agatgttcca	aatttagaaa	gcttaaggcgt	1380
gcctacagaa	aaaggaaaaaa	aggccacaaa	agttccctt	cactttcagt	aaaaataaaat	1440
aaaacagcag	cagcaaacaa	ataaaaatgaa	ataaaaagaaa	caaatgaaat	aaatattgtgl	1500
ttgtgcagca	ttaaaaaaaaaa	tcaaaataaa	aattaaatgt	gagcaaagga	aaaaaaaaaa	1560
ggcaaaagggg	gaaagaagaa	aaggggggggg	g			1591

## (2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 441 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ggcaaggcaga tacgttcgtc agcttgctcc tttctgcccc tggacgcccgc cgaagaagca 60  
 tcgttaaagt ctctcttcac cctgcccgtca tgtctaaagtc agagtctcct aaagagcccg 120  
 aacaacctgag gaaaccttcc attggaggggt tgagcttga aacaactgat gagagccctg 180  
 ggagccattt tgagcaatgg ggaacgcrcra cggactgtgt ggtaatgaga gatccaaaca 240  
 ccaagcgcctc caggggcctt gggttgtca catatgccac tgtggaggag gtggatgcag 300  
 ctatgaatgc aaggcccacac aaggtggatg gaagagttgt ggaacccaaag agagctgtt 360  
 cagagaagat ttgaaaagcc aggtgccact tacctgtgaa aaggtatttg ttggatggatt 420  
 aaggagcact tgagacatca c 441

## (2) INFORMATION ON SEQ ID NO. 25:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1131 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

cgggagggtga aatccgggttc taaccgggcc ggggctccca gcgctataaa aactttataa 60  
 acccccccgga gcccggagcag tggtaagaag aggccgagaac gaccccccggga ccgaccaaag 120  
 ccccgccgccc gctgcatccc gcgtcccaqca cctacgtccc gctggcggtcg ccgcccggcac 180  
 catgccccaaag agaaaaggctg aaggggatgc taaggggagat aaagcaaaagg tgaaggacga 240  
 accacagaga agatccgcga ggttgcgtgc taaaacctgct cctccaaagc cagagcccaa 300  
 gcctaaaaaag gccccctgcaaa agaaggggaga gaaggtacccc aaaggaaaaa aggaaaaaagc 360  
 tggatgctgqgc aaggaggggaa ataaccctgc agaaaaatgga gatgccccaaa cagaccaggc 420  
 acagaaaaagct gaagggtgctg gagatgcacca gtggaaatgtg tgcatttttg ataactgtgt 480  
 acttctggtg actgtacagt ttggaaatact attttttatac aagttttataaaaatgcaga 540  
 attttggttt actttttttt tttttttaaa agctatgttg ttggcacaca gaacacttca 600  
 ttgtttttttt tggggggagg ggcataatgtc actaataagaa tggctccaaa gctggattga 660  
 tggatggaaaaa acacccttcc cttcttagtt tgagagactt cctcttggct cccaggagga 720

gggatccct gactttgaca cacatggcca ctttggcaca aaagccttgc ggtataaaaa 780  
 aacaaaatttg tttttatgtc ctcttctccc tttccatctt tcaagcataga cttaaactccc 840  
 ttaagcccaag acatctgttg agacactgacc cctagtcatggttaccagt gtgtcaggca 900  
 atctggactt tccagtgatg ccactgagat ggcacactgtc aaaagagcag tggttccatt 960  
 tctagattgt ggatcttcag ataaattctg ccattttcat ttcaacttctt gaaagtcaagg 1020  
 gtcggcttgt gaaaagggtt taaaacaacat gctaaatgtg aaatgtcaac cctcaacttca 1080  
 aaacttttcc ctgggtcaga ggatccgatg gaggacttca attgggggtt t 1131

## (2) INFORMATION ON SEQ ID NO. 26:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

gtaccctcaa agacagagac accaagaaga atcggAACat acaggCTTg atatcaaagg 60  
 ttataaAGC caataatCTgg gaaagagaaa accgtgagac tcccAGATCT tCTCTGGTga 120  
 agtgttGTT cctgcaacga tcacgaacat gaacatcaaa ggatcgccat gaaagggtc 180  
 cctccTgCTg ctgCTGGTGT caaacCTgCT cCTGTGCCAG agcgtggccc cCTGCCCAt 240  
 ctgccccGGC gggGCTGCCC gatGCCAGGT gaccCTTCGA gacCTGTTG accGCGCCGT 300  
 cgtcCTGTCC cactacatCC atAACCTCTC cTCAGAAATG tTCAGCgAAAT tcgataAAACG 360  
 gtataccat gGCCGGGGGT tCATTACCAA gGCCATCAAC agCTGCCACA tCTCTTCCCT 420  
 tGCCACCCCCC gaagacaagg agcaAGCCCA acagatGAAT caaaaAGACT tCTGAGCCT 480  
 gatagtcAGC atattGCGAT CCTGGAATGA gCCTCTGTAT catCTGGTCA CGGAAGTACG 540  
 tggatgcaa gaaGCCCGG aggCTATCTC atCCAAAGCT gtagAGATTG aggAGCAAAC 600  
 caaaCGGCTT CTAGAGGGCA tggAGCTGAT agtcaGCCAG gttcatCCTG aaACCAAAAGA 660  
 aaatgagatC tACCTGTCT ggtcGGGACT tCCATCCCTG cAGATGGCTG atGAAGAGTC 720  
 tCGCCTTCTC GCTTATTATA acCTGCTCCA CTGCTACGC agggattcAC ataaaATCGA 780  
 caattatCTC aagCTCCTGA agtGCCGAAT catCCACAAc aacaACTGCT aAGCCACAT 840  
 ccatttCAtC tatttCTGAG aaggTCCTA atgatCCGTT ccattGCAAG tCTCTTTAG 900  
 ttgtatCTCT tttGAATCCA tGCTTGGGTG taACAGGTCT CCTCTTAAAA aataAAAact 960  
 gactcTTAG aGACATCAAa atCTAAAAAa ACTTAATGGG CGGGGCGCAG tggCTCATGG 1020  
 ctgtggTCCC ggcactTTGG gaggCCGAGG caggCGGATC aggAGGTcAG g 1071

## (2) INFORMATION ON SEQ ID NO. 27:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 896 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

gtgaccggct cagaccggcc ctggagacaa aaggggccgc ggccggccgg a cggggacggg 60  
 cccggcgccgg gagggagcga agagcgcggc caqcqagcga qatgcagcac cgaggcttc 120  
 tcctccctcac cctccctcgcc ctgctggcgc tcacccctccgc ggtcgccaaa aagaaagata 180  
 aggtgaagaa gggcgccccgg gggagcgaat ggcgtgatgg ggcctggggg ccctgcaccc 240  
 ccagcagcaa ggattgcggc gtgggtttcc gcgaggggcac ctgcggggcc cagacccagc 300  
 gcatccgggtc cagggggccc tgcaactggg agaaggagtt tggagccgac tgcaagtaca 360  
 agtttggagaa ctgggggtgcg tggatgggg gcacaggcac caaagtccgc caaggcacc 420  
 tgaagaaggc ggcgtacaat gtcgtgcgc aggagaccat ccgcgtcacc aagccctgca 480  
 cccccaagac caaagcaaaag gccaaagccca agaaaggggaa gggaaaggac tagacgcca 540  
 gcctggatgc caaggagccc ctgggtgtcac atggggcctg gcccacgccc tcctctccc 600  
 aggccccgaga tggacccac cagtgccttc tggatgtcg ttagctttaa tcaatcatgc 660  
 cctgccttgt ccctctcaact cccccagcccc accccctaagt gcccaaagtg gggagggaca 720  
 agggatctg ggaagttga gcctccccc aagcaatgtg agtcccagag cccgctttt 780  
 ttcttccca caattccatt actaagaaac acatcaaata aactgacttt ttccccccaa 840  
 aaaaagctct tcttttttaa tataaaaaaa aaaaaaaaaa aaaaaaaaaa aagaaa 896

## (2) INFORMATION ON SEQ ID NO. 28:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ttttcatttt tttttttttt ttttctcag ttcaagttta atacaaacta caaaagatta 60  
 atgggttgct ctactaatac atccataaaaa ccagtagcct gcccacaacg ccaactcagg 120  
 ccattccctac caaaggaaga aaggctggc tctccacccct ctgttagggaa ggcctgcctt 180  
 gtaagacacc acaattccgc tgaatctgaa gtcttgcgtt ttactaatgg aaaaaaaaaa 240  
 tacagaagag gttttgttct catggctgc caccgcagcc tggcactaaa acagcccaagc 300  
 gctcacttct gcttggagaa atattctttt ctcttttggg catcaggctt gatggatca 360  
 ctgccaggtt tccagccagc tgggcacact tccccatgtt tgcgtgcgc cggaaaggcc 420  
 tgaacttagtc tcaaagtcc atccacagag cggccaaacag ggaaggcatt tacagtgc 480  
 tgccgaagaa tacccttatac atcaatgata aaaaggcccc tgaacgagat gcttcatca 540  
 gcctttaaga ccccataatac ctgagcaatg gtgcgttcg ggtctgatac caaaggaatg 600  
 ttcatgggtc ccagtccccc ttgtttcttta ggtgtattga cccatgttagt aqacagaag 660  
 tgagaatcca cagaagcacc aatcaactgg cagttggat tttaaattc ttctgcctt 720  
 tcactgaaag caatgatcc cgtggggcac acaaagggtga agtcaagagg gtaaaagaag 780  
 aacacaacat attttccctt ttagtcagac aggctgatata tttaaactg accatctggc 840  
 ataacagctg tggcttggaa gttgggggca gggcgccaa ttttagcatt tcctgaagac 900  
 atcttcctat cagcagtccc aacacaagtc gcaaaaaacta accaccgaca ccaggcaaga 960  
 acaagacgcg caagagctct ccggggcgct gccttatacg ccagtagggc tctgcacal 1020  
 gtcggaaacgg acgggggtgc cgagtagga 1050

## (2) INFORMATION ON SEQ ID NO. 29:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 581 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

caaggcttccct tctggcaaca ggcgtgggtc acqctctcgc tcggtcttc tgccgccc 60  
 ttgggtccgc gttccctgca caaaatqccc ggcgaacacc aqaaaccgtc cctgctacagl120  
 agcaaggagtt gcccgcagccc caggctgaga caaggqtctqq aacaqaatct gacagtgatg180  
 aatcaqtacc agagcttcaa gaacaggatt ccaccaggc aaccacacaa caagcccagc240  
 tggcggcagc aqctgaaatc qatqaagaac caqtcagtaa aqcaaaaacag aqtcggagtg300  
 aaaagaaggc acggaaggct atgtccaaac tgggtcttcg qcaggttaca ggagtacta360

gagtcaactat ccggaaatct aagaatatcc tctttgtcat cacaacaaccg gttgtctaca420  
 agagccctgc ttcaagatacg tacatagttt ttggggaaagc cagatcgaag attatcccag480  
 caagcacaac tagcagctgc tgagaagtca agttcaggtg aactgtctca acgttcaggaa540  
 aaccccccggc ttccactgta gagggggaggt aagggggaggg t 581

## (2) INFORMATION ON SEQ ID NO. 30:

## (i) SEQUENCE CHARACTERISTIC:

---

- (A) LENGTH: 264 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

gggactatgt tggagcctg cggaaagaat ttgtgtgggg actgtggca gtgaatgcgt 60
tgggaacaat atggaaaact gggagctgcc ctcagtttct ccccaagttt gactcacttt120
cggggtgtcc caaaagccctg attccagggc ctgctagccc gaccccggtg acgcctccac180
ccgcgcctgg ccccaagccctt caccgcgtat cgccgccttc cggggcacac cttccgcac240
aaaacacagccg gggggcgccg agac 264

```

## (2) INFORMATION ON SEQ ID NO. 31:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 111 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

cggcgaatca cttataaaatg gcgcgcgaagc aggagcccga aggctaaatt gcaggagggg 60
tgagcgaatg cttgtgtttttc atgggcctct tacgttcatg aggccaaatgt 111

```

## (2) INFORMATION ON SEQ ID NO. 32:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 76 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

00000000000000000000000000000000

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

PFCEETKTER LWPRCRPPA VGFSTQNPGV GDSESNLFSL PFLGSKANPI PTHWSSALIF60  
NLPSPPFQNT HIPEQN 76

(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 72 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

SSFLFSFQTQ FHKNRDKVF SSRQAKPFPH HQSILKIHEE VERSVSGRLK GSSSSNPTAA60  
EKIEIEILKI TS 72

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 70 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

KKLDYFCAEI KNSHCKTKIK IAQIRKPGGA KCQVSKVHFF SLSKRSSTKT ARIKF SVADK60  
QSPFHIIINQS 70

## (2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

SSGPAPGCSP FAGTRKNFPS MVVLERTFLK INYIFLCIPM EFQFIRCSPW P9QNTEVIPA60

## (2) INFORMATION ON SEQ ID NO. 36:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ASGVHTETHR YNLLSAKSRK KGWGYLGWLG FDFLLVCLFC TKTVLSFEYR RDISIYMLSN60  
QDG 63

## (2) INFORMATION ON SEQ ID NO. 37:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 170 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ARAARAQQTP HLTLPAVLQT LHLLRPTLSP ESKLEWNNDI PEVNHLNSEH WRKTEKWTGH 60  
 EETNHLETDF SGDGMTELEL GPSPLQPIR RHPKELPQYG GPGKDIFEDQ LYLPVHSDGI120  
 SVHQMFMTMAT AEHRSNNSIA GKMLTKVEKN HEKEKSQHLE GSASSSLSSD 170

(2) INFORMATION ON SEQ ID NO. 38:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 144 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

ARAPTLDMRF RRRLSADPHQ TQRNSAEARG TMDGRVQLMK ALLAGPLRPA ARRWRNPIPF 60  
 PETFDGDTDR LPEFIVQTCS YMFDVDENTFS NDALKVTFLI TRLTGALQW VIPYIRKESP120  
 LLNDYRGFLA EMKRVFGWEE DEDF 144

(2) INFORMATION ON SEQ ID NO. 39:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 178 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

HSLGRAPVET LAVATGTANS SQSTRPQARG SPGLEVLVLL PSKDSDLHLGQ KAPVIIIEQGA 60  
 LLPDVGDHPL QGWPREAGDE ERHLQGVVGE RVLVHEHVGA RLHDELRESV GISVKRLGKG120  
 NRVPPATRRG PEGPGQEGLH QLHPTVHRAA RLGVSLGCV GVSAKASPEA HVEGGGPG 178

## (2) INFORMATION ON SEQ ID NO. 40:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 89 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

KLTGINTGCR NMLALCIRGH AQQIQEIYLA TFSRKGTGAI IHYILEVFLG FFFFFLRLQSC60  
CIAQAGSVVA QSQLIASSIT QGLSNPPTL

89

## (2) INFORMATION ON SEQ ID NO. 41:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

IVTWRKVRPMS LCQRPPPFVRLGIFRLLKGL AHIRCDLFLP VVMEGHICQS LESAKAGTRF60  
PGPQWGCAKP RELGCKFVKN QHHVWQLSIG ARSLP

95

## (2) INFORMATION ON SEQ ID NO. 42:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 154 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CQLVFRIQTD GSYWSLGLTS SGNITFSWAE MLLPALKQHS VLKTSWQAPG SNTQLPNMML 60  
 ILHEFATQFS RVCTPPLWAG EPGPGLRRLQ ALADVALHNN GNEKVT PYVR QALKES EYFPN120  
 PHKRRGTLAK THGNFPPSND LDRRATQDSP SCSV

154

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 79 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

LASTLGVETC LPYVSEDMMS RSKRYIWQLF LEKAHWVSFI TFLSFFGFFF FFFETVLLYC60  
 PGWSVVAQSQ LIASSITQA

79

(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 82 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CQLVFRIQTD GSYWSLGLTS SGNITFSWAE MLLPALKQHS VLKTSWQAPG SNTQLPNMML60  
 ILHEFATSWL PRLQHSAVGT QS

82

## (2) INFORMATION ON SEQ ID NO. 45:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

RGSKDRNSGQ GSGSYGQLSC RGFSQFSRV CTPPLWAGEP GPGLRLQAL ADVALHNNGN60  
EKVTPYVR 68

## (2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 87 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

DYVVSLRKKF VWGLWAVNAL GTIWKTGSCP QFLPKLDSLS GCPKSLIPGP ASPTPVTPPP60  
APGPSLHPRS EPGSAHPPPPE NSRRAAR 87

## (2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 51 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

QALESGFWDT PKVSPTWGET EGSSQFESILF PTHSLPTVPT QTSFAGSQHS P

51

(2) INFORMATION ON SEQ ID NO. 48:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

RRITYKWRSS RSPKAKLQEG

20

(2) INFORMATION ON SEQ ID NO. 49:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 36 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GESLINGAEA GARRLNCRRG ERMLCFHGPL TLMRQS

36

## (2) INFORMATION ON SEQ ID NO. 50:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

KHSIRSPLLQ FSLRAPASAP FISDSSP

26

## (2) INFORMATION ON SEQ ID NO. 51:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

EAHESTAFAH PSCNLAFGLL LRRHL

25

## (2) INFORMATION ON SEQ ID NO. 52:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3665 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

**(C) ORGAN:**

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GGCCCATTTG	TGAAGAGACG	AAGACTGAGC	GGTTGTGGCC	CGCTTGCCGA	CCTCCAGCAG	60
CAGTCGGCTT	CTCTACGCAG	AACCCGGGAG	TAGGAGACTC	AGAAATCGAA	TCTCTCTCC	120
CTCCCCTTCT	TGGGCAGCAA	GGCGAACCCC	ATCCCCTACTC	ACTGGAGCTC	AGCTTGATT	180
TTTAACCTCC	CTTCCCCCAC	CTTCCAGAAC	ACACACATTC	CATTCAAAAA	CTGATTTAT	240
AAAGACATT	TAAACATAAT	GATGCAACTT	GGTGTGCACT	ACAGCAAATG	TACAGGTGTT	300
TTTTTTTAA	TTGTTTCCAA	AACCAGGACC	TGGATTTAAG	ATGTAATT	AAAATTCT	360
ATTTCTATT	TTTCTGCAGC	AGTGGGTTA	GAGGAGGAGG	AGCCTTTAG	CCTCTCATAA	420
ACTGACCTCT	CTACTCCCTC	GTGTATTTT	AAGATTGATT	GATGATGTGG	AAAGGGCTT	480
GCTTGTCTGC	TACTGAAAAC	TTTATCCTGC	GGTTTTGTG	GAAACTGCTT	TTGGAAAGAG	540
AAAAGAAATG	AACTTTACTG	ACTTGACATT	TTTGACCTC	CGGTTTTCT	AATCTGGGCT	600
ATTTTATTT	TTGTTTTTTT	ACAGTGAGAT	TTTTTGATC	TTCAGCTTAC	ATTTTCGGGC	660
TTTGTGAGGA	AACCTTTAC	CATCAAACAC	GATGGCCAGC	AACGTTACCA	ACAAGACAGA	720
TCCTCGCTCC	ATGAACCTCC	GTGTATTCAT	TGGGAATCTC	AACACTCTG	TGGTCAAGAA	780
ATCTGATGTG	GAGGCAATCT	TTTCGAAGTA	TGGCAAAATT	GTGGGCTGCT	CTGTTCATAA	840
GGGCTTGCC	TTCGTTCACT	ATGTTAATGA	GAGAAATGCC	CGGGCTGCTG	TAGCAGGAGA	900
GGATGGCAGA	ATGATTGCTG	GCCAGGTTT	AGATATTAAC	CTGGCTGCAG	AGCCAAAAGT	960
GAACCGAGGA	AAAGCAGGTG	TGAAACGATC	TGCAGCGGAG	ATGTACGGCT	CCTCTTTGA1020	
CTTGGACTAT	GACTTTCAAC	GGGACTATT	TGATAGGATG	TACAGTTACC	CAGCACGTGT1080	
ACCTCCTCCT	CCTCCTATTG	CTCGGGCTGT	AGTGCCCTCG	AAACGTCAGC	GTGTATCAGG1140	
AAACACTTCA	CGAAGGGGCA	AAAGTGGCTT	CAATTCTAAG	AGTGGACAGC	GGGGATCTTC1200	
CAAGTCTGGA	AAAGTTGAAAG	GAGATGACCT	TCAGGCCATT	AAGAAGGAGC	TGACCCAGAT1260	
AAAACAAAAA	GTGGATTCTC	TCCTGGAAAA	CCTGGAAAAA	ATTGAAAAGG	AACAGAGCAA1320	
ACAAGCAGTA	GAGATGAAGA	ATGATAAGTC	AGAAGAGGAG	CAGAGCAGCA	GCTCCGTGAA1380	
GAAAGATGAG	ACTAATGTGA	AGATGGAGTC	TGAGGGGGGT	GCAGATGACT	CTGCTGAGGA1440	
GGGGGACCTA	CTGGATGATG	ATGATAATGA	AGATCGGGGG	GATGACCCAGC	TGGAGTTGAT1500	
CAAGGATGAT	AAAAAAGAGG	CTGAGGAAGG	AGAGGATGAC	AGAGACAAAGG	CCAATGGCGA1560	
GGATGACTCT	TAAGCACATA	GTGGGGTTA	GAAATCTTAT	CCCATTATT	CTTACCTAG1620	
GGGGTTGCT	AAGATCAAAT	TTTCAACCAG	ATCCTCTCCC	CTAGTATCTT	CAGCACATGC1680	
TCACTGTTCT	CCCCATCCTT	GTCCCTCCCA	TGTTCATTTAA	TTCATATTGC	CCGGCGCCCTA1740	

GTCCCATTTT CACTTCCTTT GACGCTCCTA GTAGTTTGT TAAGTCTTAC CCTGTAATTT1800  
 TTGCTTTAA TTTTGATAACC TCTTTATGAC TTAACAATAA AAAGGATGTA TGCTTTTAT1860  
 CAACTGTCTC CAAAATAATC TCTTGTATG CAGGGAGTAC AGTTCTTTC ATTCAACAT1920  
 AAGTCAGTA GTTGCTTCCC TAACTGCAAA GGCAATCTCA TTTAGTTGAG TAGCTCTTGA1980  
 AAGCAGCTTT GAGTTAGAAG TATGTGTGTT ACACCCCTCAC ATTAGTGTGC TGTGTGGGC2040  
 AGTCAACAC AAATGTAACA ATGTATTTT GTGAATGAGA GTTGGCATGT CAAATGCATC2100  
 CTCTAGAAAA ATAATTAGTG TTATAGTCTT AAGATTGTT TTCTAAAGTT GATACTGTGG2160  
 GTTATTTTG TGAACAGCCT GATGTTGGG ACCTTTTTC CTCAAAATAA ACAAGTCCTT2220  
 ATAAACCAG GAATTGGAG AAAAAAAA AAAAAAATT TTTATTTTG TATTTTATTA2280  
 TTGTTTACTT CAAACTTGT TTTACAGCGT CCTCCACAAA ACCTCTAGAA TGCACTAGAT2340  
 ATATTTTCT TGGAGTCATA ATCATGATGC ATACCAACAC AACACTACTC AAATTATATT2400  
 TCATTGAGAT GCATGTTGCA TTGAGGAGTC AACTTGACAT AGAGTGGAGA CTTTTCAAA2460  
 ATGGCTTTA CATCCTAATG AAAGTTGGG AAGTATATCC TCTCTGCCTT TTCATCAGTG2520  
 CTTTGTGGTC CAGCTGGCAC CCTTCTGAG GTTTGTGTT TGTGCTAAAT GTTTTGTCC2580  
 TTAAATAGGA GAGGCTCAAA AACATCAAGA TTTCAGAAA ATGGCGACAC TGGCATAATG2640  
 GAACCCCCCT GCTTCTATTT TGTCTTTTA ATTACTATT ATAGCCCCAG TTACCTTCTG2700  
 AATTCTGAAG TGTATATACC TCCATGTTCC TGAAAACAAG AAAACTCTTA CTTCTGATA2760  
 TTCCATAGAC TGCCCTTCCA GGTGATTGAG AACATAGAGA ATGTTACACA TTTATTTAC2820  
 TCTAAATGAT CTTTACCCC TGTAGCTAA TCTTGTGTT TTCTCTAACT TTATTAATTA2880  
 CAGTGATTGC ATTTTAGCA TCCAGTTGTA AGATGAATAT ATAAACAGC TACCAAGTGT2940  
 GGTGATACCT CATCCTTGAA AGGCTTAGTT CATTGTGTT TTATACTTCA GTTTTCCAG3000  
 CATAGCAGAA AATGCCGCTT ATAATTTTG TGCACACAAA CCTTGGAAAT CCCCTGTAA3060  
 GTTGTATGG TTTCATAGCA TGCGGCACTG GCCCCTTTTT CATCCCACTC ATTACAGGCA3120  
 AAACCCATGT CTTATTTATG AGGATTTAT AGATCATT TTGTAAACAGG TGACAAAAGC3180  
 AGAAAAGAAT GAAGAGGCTG AAGTATGAAC TACCCCTTGA GCCCATATAC ATGATATAGG3240  
 CAATTCTTT TGTATGTTAA TTCAGTCAAA AATACTACCC ACTTGTGTT TTCTAATCTG3300  
 ATGTGAGCTC ATGTTACACA GACTTTAGT AAGTAACCCG TGACTAGAAA ATAAACTGGA3360  
 TGCTTAGGAG AGAGTGTCA GATGATAAGA TGCTAATAAA ACCTGTTAA TATTATTGTT3420  
 AGCTGTAAGT TTTTGGAAA TACTGAACAA ATTAGTCCAC AATCAAGTGT CTACTTTCC3480  
 CTTCACTGTA GGGCCTCTCC CTGCACAGAG CAGTCTGTT AGCTGTGAAC ACCACAATCT3540  
 GCAGATGTTCA AAGTCCCTTA CATAAAATGG CATAGTATTT ATATGTAACC TATGCATATT3600  
 CTCCTGTATA TTTAAATCA TCTCTACATT AAAATACCTG ATAAAATCTA AATAAAAAA3660  
 AAAAAA

3665

## (2) INFORMATION ON SEQ ID NO. 53:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 301 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GNLYPSNTMA SNVTNKTDPR SMNSRVFIGN LNTLVVKSD VEAIFSKYKGK IVGCSVHKGF 60  
 AFVQYVNERN ARAAVAGEDG RMIAGQVLDI NLAAEPKVNR GKAGVKRSAA EMYGSSFDLD120  
 YDFQRDYDR MYSYPARVPP PPPIARAVVP SKRQRVSGNT SRRGKSGFNS KSGQRGSSKS180  
 GKLKGDDLQA IKKELTQIKQ KVDLLENLE KIEKEQSKQA VEMKNDKSEE EQSSSVKKD240  
 STNVKMESEG GADDSAEEGD LLDDDDONEDR GDDQLELIKD DEKEAEEGED DRDKANGEDD300  
 S

301

## (2) INFORMATION ON SEQ ID NO. 54:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

ESSSPLALSL SSSPSSASFS SSLINSSWSS PRSSLSSSS RSPSSAESSA PPSDSIFTLV 60  
 SSFFTELLC SSSDLSFFIS TACLLCSFSI FSRFSRREST FCFIWVSSFL MA 112

## (2) INFORMATION ON SEQ ID NO. 55:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

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TRNLEKKKKK NFLFLYFIIV YFKLCFTASS TKPLECTRYI FLGVIIMMHT NTTLLKLYFI 60  
 EMHVALRSQD DIEWRLFQNG FYILMKVWEV YPLCLFISAL WSSWHPF 107